GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 01:06:32 ; Search time 1354 Seconds
(without alignments)
6014.199 Million cell updates/sec

Title: US-09-924-946-1
Perfect score: 3616
Sequence: 1 gattatgttgggggtcggc.....gttgctcattatggactgct 3616

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3616	100.0	3616	24	AAD30517	Human endothelial
	2	3436	95.0	3532	24	AAI67789	Human lysyl oxidas
	3	2844.4	78.7	2976	24	ABA96419	Human 47765 lysyl
	4	2597.2	71.8	2603	24	AAD33480	Human drug metabol
	5	2263.2	62.6	2268	24	ABA96420	Human 47765 lysyl
	6	1918.8	53.1	3767	21	AAA96737	Polynucleotide iso
	7	1718.2	47.5	1782	21	AAC90030	Clone HOHEC84 codi
	8	1718.2	47.5	1782	21	AAC93436	Human secreted pro
	9	1711.4	47.3	1781	21	AAC90026	Clone HOHEC84 codi
	10	853.8	23.6	3748	23	ABV23110	Human prostate exp
	11	853.8	23.6	3748	23	ABV28948	Human prostate exp
	12	849	23.5	3432	24	ABQ88183	Human osteoblast d
	13	847.4	23.4	2325	24	ABA95142	Human LOR-1 protei
	14	811.6	22.4	3467	22	AAH98714	Human EST-derived
	15	787.4	21.8	2714	22	AAD19235	Human lipid metabo
	16	765.8	21.2	2262	21	AAA47799	Human lysyl oxidas
	17	765.8	21.2	2262	22	AAI67193	Nucleotide sequenc
	18	765.8	21.2	2785	24	AAD24786	Human secreted pro
	19	765.8	21.2	2920	21	AAA47798	Human lysyl oxidas
	20	765.8	21.2	3121	24	AAI67788	Human lysyl oxidas
	21	764.8	21.2	2262	24	ABA95143	Human lysyl-oxidas
	22	762.6	21.1	5059	22	AAD19230	Human CG153 (or C5
	23	709	19.6	2420	22	AAD19222	Human CG153 (or C5
	24	706.2	19.5	3198	22	AAH81777	Human differential
	25	706.2	19.5	3198	24	ABQ88184	Human osteoblast d
	26	706.2	19.5	3198	24	AAI67787	Human lysyl oxidas
	27	681.4	18.8	2860	21	AAA61292	Human secreted pro
	28	641.4	17.7	2130	21	AAA61266	Human secreted pro
	29	581	16.1	4552	22	AAD19231	Human CG153 (or C5
c	30	502.2	13.9	597	24	ABL79085	Human ovarian canc
c	31	450.2	12.5	460	24	ABN94644	Gene #1142 used to
	32	403	11.1	1419	24	ABK15350	cDNA encoding huma
c	33	322	8.9	327	21	AAC68730	Human TSC33 cDNA.
	34	239.6	6.6	513	22	AAH81629	Human differential
	35	199.8	5.5	1536	23	ABL07603	Drosophila melanog
c	36	199.2	5.5	2476	20	AAX87159	Human protease HUP
	37	191.6	5.3	1725	24	ABA95144	Human lysyl-oxidas
	38	191.6	5.3	2328	24	AAI67786	Human lysyl oxidas
	39	184.6	5.1	187	21	AAC68729	Human TSC33 cDNA f
	40	159.4	4.4	643	23	ABV44017	Human prostate exp
	41	146.6	4.1	1089	23	ABL03581	Drosophila melanog
	42	145.8	4.0	1251	19	AAV19962	Homo sapiens lysyl
	43	145.8	4.0	1254	24	ABA95145	Human lysyl-oxidas
	44	145.8	4.0	2947	22	AAL26448	Human breast cance
	45	145.8	4.0	2947	22	AAL26765	Human breast cance

ALIGNMENTS

RESULT 1
AAD30517
ID AAD30517 standard; cDNA; 3616 BP.
XX
AC AAD30517;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human endothelial estrogen regulated (EER)-7 cDNA.
XX
KW Human; lysyl oxidase; LO gene; endothelial estrogen regulated gene; AAA;
KW abdominal aortic aneurysms; EER-7 gene; myocardial infraction; elastin;
KW fibrotic disease; gene therapy; cardiant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..2390
FT /*tag= a
FT /product= "Human EER-7 protein"
XX
PN WO200212470-A2.
XX
PD 14-FEB-2002.
XX
PF 08-AUG-2001; 2001WO-US24942.
XX
PR 08-AUG-2000; 2000US-223763P.
PR 15-DEC-2000; 2000US-255838P.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX

PI Evans MJ, Scicchitano MS, Bapat AR, Beer E, Bhat RA, Ferris E;
PI Mastroeni R, Zhang J, Karathanasis SK;
XX
DR WPI; 2002-227150/28.
DR P-PSDB; AAE19380.
XX
PT Novel isolated endothelial estrogen regulated gene protein comprising
PT lysyl oxidase activity and conserved catalytic domain of lysyl oxidase,
PT useful as target to treat abdominal aortic aneurysms, myocardial
PT infarction -
XX
PS Claim 12; Page 61-62; 68pp; English.
XX
CC The patent discloses novel lysyl oxidase (LO) genes, termed endothelial
CC estrogen regulated (EER)-7 genes and their corresponding proteins. The
CC invention also relates to an assay system to identify compounds that
CC selectively modulate EER7 protein activity by interaction with estrogen
CC receptors. Stimulation of LO enzyme activity of EER-7 acts as a target
CC for abdominal aortic aneurysms (AAA) and myocardial infractions. Increase
CC in EER-7 lysyl oxidase activity increases elastin cross-linking in the
CC inner elastic lamina which prevents development of aneurysms. Increased
CC EER-7 is also useful to increase collagen cross-linkings which increase
CC tensile strength of vessel wall which also prevents aneurysms. Myocardial
CC infraction is prevented by inhibiting rupture of fibrous cap that covers
CC plaque in the coronary vessels. Increased tensile strength of the cap,
CC resulting from increased LO activity helps preventing the infractions.
CC Inhibition of LO activity is useful for treating fibrotic diseases.
CC Stimulation of EER-7 proteins are useful for treating patients with
CC estrogen-related disease states. Genetic variants of EER-7 can be
CC detected to diagnose an EER-7 associated disease such as AAA or
CC myocardial infarction. EER-7 polynucleotides are useful in gene
CC therapy. The present sequence is a cDNA encoding human EER-7 protein.
XX
SQ Sequence 3616 BP; 813 A; 997 C; 1065 G; 741 T; 0 other;

Query Match 100.0%; Score 3616; DB 24; Length 3616;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     121 TGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCTC 180
Db     121 TGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCTC 180

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TAGTTAAGGATGGAACCTGGGAAAGGCCACCATTCCTGCTTGATGGGGCTCTGATTTGCT 3480

Qy   3481 CTTGCTCAAGTGGAATAAAACCCCATGGTCTTCTTGACATGATTCTTGATCTTTTCTCCA 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CTTGCTCAAGTGGAATAAAACCCCATGGTCTTCTTGACATGATTCTTGATCTTTTCTCCA 3540

Qy   3541 CTGAGACACACTTAAGTGATGATCCTTACAGGACTGACACCCTAATGCCAATAAAAGTTG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CTGAGACACACTTAAGTGATGATCCTTACAGGACTGACACCCTAATGCCAATAAAAGTTG 3600

Qy   3601 CTCATTATGGACTGCT 3616
          ||||||||||||||||
Db   3601 CTCATTATGGACTGCT 3616
```

RESULT 2
AAI67789
ID AAI67789 standard; cDNA; 3532 BP.
XX
AC AAI67789;
XX
DT 27-FEB-2002 (first entry)
XX

```
DE   Human lysyl oxidase-like (LOXL4) protein encoding cDNA.
XX
KW   Lysyl oxidase; lysyl oxidase-like; LOXL; LOX; neuroprotective; nootropic;
KW   dermatological; hepatotropic; cytostatic; antidote; LOXL4; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             81..2312
FT                   /*tag= a
FT                   /product= "LOXL4"
XX
PN   WO200183702-A2.
XX
PD   08-NOV-2001.
XX
PF   03-MAY-2001; 2001WO-US14472.
XX
PR   03-MAY-2000; 2000US-201587P.
XX
PA   (UYHA-) UNIV HAWAII.
XX
PI   Csiszar K,  Boyd CD,  Kim Y,  Le Saux CJ,  Fong SFT;
XX
DR   WPI; 2002-041491/05.
DR   P-PSDB; AAG66060.
XX
PT   Novel copper-dependent lysyl oxidase-like proteins, nucleic acids
PT   encoding the protein for diagnostic assays and identifying modulators
PT   useful for treating cancer, skin, copper-related, pulmonary or hepatic
PT   disorders -
XX
PS   Claim 6; Page 78-79; 82pp; English.
XX
CC   The invention provides lysyl oxidase-like (LOXL) polypeptides and
CC   polynucleotides encoding them. The LOXL proteins (LOXL3 and LOXL4) can be
CC   expressed by standard recombinant methodology. The LOXL polypeptides are
CC   useful for identifying their modulators which can be used for treating a
CC   disorder associated with LOX or LOXL polypeptide activity, including
CC   disorders related to extracellular matrix materials, a cell migration,
CC   cell proliferative disorder, skin, vascular system, developmental,
CC   skeletal, neurological, hepatic system, copper-related, pulmonary system
CC   disorders or lathyrism disorder and cancer in a subject. The LOXL
CC   polynucleotides are useful as probes and primers. The LOXL polypeptides
CC   are useful in bioassays, for the production of antibodies, useful for
CC   diagnostic assays to determine expression levels and localization of
CC   LOXL3 and LOXL4 proteins and other proteins of the LOX gene family in
CC   various tissue samples from healthy or infirm subjects and to purify the
CC   proteins. The antibodies are therapeutically useful to counteract or
CC   supplement the biological effect of LOXL proteins in vivo. The present
CC   sequence represents a human-derived LOXL4 protein encoding cDNA.
XX
SQ   Sequence 3532 BP; 784 A; 991 C; 1036 G; 721 T; 0 other;

  Query Match             95.0%;  Score 3436;  DB 24;  Length 3532;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches 3497;  Conservative    0;  Mismatches   20;  Indels   39;  Gaps    1;

Qy         55 GACTTCAAGCCCCCTCTTTCCTAGCCTGGACAGGTATCTTGGCCTCAGCTGTCCTTGAAG 114
              | |  | |||||    |  | |     |  ||||||||||||||||||||||||||||
Db         16 GCCGCCCAGCCCCGGACTGTCGCGCTCCATCTGGTATCTTGGCCTCAGCTGTCCTTGAAG 75

Qy        115 TCACCATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGC 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 TCACCATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGC 135

Qy        175 CCCCTCCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGA 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 CCCCTCCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGA 195

Qy        235 GCAAGCCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTG 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GCAAGCCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTG 255

Qy        295 ATGACAACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTG 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 ATGACAACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTG 315

Qy        355 CCTTGACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACA 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CCTTGACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACA 375

Qy        415 ATGTGCGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAG 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATGTGCGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAG 435

Qy        475 TCAGTGACTGCAGTCACTCAGAAGACGTAGGGGTGATATCCCACCCCCGGCGCCATCGTG 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TCAGTGACTGCAGTCACTCAGAAGACGTAGGGGTGATATCCCACCCCCGGCGCCATCGTG 495

Qy        535 GCTACCTTTCTGAAACTGTCTCCAATGCCCTTGGCCCCAGGGCCGGCGGCTGGAGGAGG 594
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTACCTTTCTGAAACTGTCTCCAATGCCCTTGGCCCCAGGGCCGGCGGCTGGAGGAGG 555

Qy        595 TGCGGCTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATACCCCAGTGACCGAGGGAGCCG 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCGGCTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATACCCCAGTGACCGAGGGAGCCG 615

Qy        655 TGGAGGTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACA 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 TGGAGGTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACA 675

Qy        715 ACAGCAGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACT 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACAGCAGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACT 735

Qy        775 ACTACAGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGA 834
              |||||                                       ||||||||||||||
Db        736 ACTAC---------------------------------------AGGCTGAAGAGCCTGA 756

Qy        835 CGAATAAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGG 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CGAATAAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGG 816

Qy        895 CCAACTGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTG 954
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        817 CCAACTGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTG 876

Qy        955 GCATGCATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGC 1014
              ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        877 GCATGCACGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGC 936

Qy       1015 CACAACGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGG 1074
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 CACAACGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGG 996

Qy       1075 TGGGCGAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACA 1134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 TGGGCGAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACA 1056

Qy       1135 GGTGGAACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGG 1194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 GGTGGAACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGG 1116

Qy       1195 AGGCCCTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGC 1254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 AGGCCCTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGC 1176

Qy       1255 GCTGCAGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATG 1314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GCTGCAGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATG 1236

Qy       1315 GTTGCCAACATGAGAATGCTGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGA 1374
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1237 GTTGCCAACATGAGAATGATGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGA 1296
```


Qy 1375 ATCAGGTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCTATTGGAGGTGCAGGTGG 1434
Db 1297 ATCAGGTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCTATTGGAGGTGCAGGTGG 1356
Qy 1435 AGGTGAACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAG 1494
Db 1357 AGGTGAACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAG 1416
Qy 1495 CCATGGTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCT 1554
Db 1417 CCATGGTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCT 1476
Qy 1555 GGTTCTGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAG 1614
Db 1477 GGTTCTGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAG 1536
Qy 1615 GCACAGAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTG 1674
Db 1537 GCACAGAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTG 1596
Qy 1675 GCGGGCGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACG 1734
Db 1597 GCGGGCGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACG 1656
Qy 1735 CCCAGCTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTG 1794
Db 1657 CCCAGCTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTG 1716
Qy 1795 CCCACGAGGAGAACTGCCTCTCCAAGTCTGCGGATCACATGGACTGGCCCTACGGATACC 1854
Db 1717 CCCACGAGGAGAACTGCCTCTCCAAGTCTGCGGATCACATGGACTGGCCCTACGGATACC 1776
Qy 1855 GCCGCCTATTGCGCTTCTCCACACAGATCTACAATCTGGGCCGGACTGACTTTCGTCCAA 1914
Db 1777 GCCGCCTATTGCGCTTCTCCACACAGATCTACAATCTGGGCCGGACTGACTTTCGTCCAA 1836
Qy 1915 AGACTGGACGCGATAGCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGG 1974
Db 1837 AGACTGGACGCGATAGCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGG 1896
Qy 1975 TCTTCACCCACTACGACCTCCTCACTCTCAATGGCTCCAAGGTGGCTGAGGGGCACAAGG 2034
Db 1897 TCTTCACCCACTACGACCTCCTCACTCTCAATGGCTCCAAGGTGGCTGAGGGGCACAAGG 1956
Qy 2035 CCAGCTTCTGTCTGGAGGACACAAACTGCCCCACAGGACTGCAGCGGCGCTACGCATGTG 2094
Db 1957 CCAGCTTCTGTCTGGAGGACACAAACTGCCCCACAGGACTGCAGCGGCGCTACGCATGTG 2016
Qy 2095 CCAACTTTGGAGAACAGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACATTG 2154
Db 2017 CCAACTTTGGAGAACAGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACATTG 2076
Qy 2155 ATTGCCAGTGGGTGGATATCACAGATGTGGGCCCCGGGAATTATATCTTCCAGGTGATTG 2214
Db 2077 ATTGCCAGTGGGTGGATATCACAGATGTGGGCCCCGGGAATTATATCTTCCAGGTGATTG 2136
Qy 2215 TGAACCCCCACTATGAAGTGGCAGAGTCAGATTTCTCCAACAATATGCTGCAGTGCCGCT 2274
Db 2137 TGAACCCCCACTATGAAGTGGCAGAGTCAGATTTCTCCAACAATATGCTGCAGTGCCGCT 2196
Qy 2275 GCAAGTATGATGGGCACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATACCCAG 2334
Db 2197 GCAAGTATGATGGGCACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATACCCAG 2256
Qy 2335 CCAATGCAGAACTCTCCCTGGAGCAGGAACAGCGTCTCAGGAACAACCTCATCTGAAGCT 2394
Db 2257 CCAATGCAGAACTCTCCCTGGAGCAGGAACAGCGTCTCAGGAACAACCTCATCTGAAGCT 2316
Qy 2395 GTCACTGCACACTCCTAGCTGCTGCCGATACACCAGATACCTCAGCTTATTGGAGCCATG 2454
Db 2317 GTCACTGCACACTCCTAGCTGCTGCCGATACACCAGATACCTCAGCTTATTGGAGCCATG 2376
Qy 2455 CCCTTCACAGAGTCCCAACTCAGAGGAAAAGGGCCAGTGCCAAGGGGCACCAAGAACCTG 2514
Db 2377 CCCTTCACAGAGTCCCAACTCAGAGGAAAAGGGCCAGTGCCAAGGGGCACCAAGAACCTG 2436
Qy 2515 CTCAGGAAGCCTTTTGATGGCAAGATCACCAATCCAGATGGTATTGCTCCCTCAGGATGG 2574
Db 2437 CTCAGGAAGCCTTTTGATGGCAAGATCACCAATCCAGATGGTATTGCTCCCTCAGGATGG 2496
Qy 2575 CTCTGGGCCTGCCCCTAAGGGCCTGTGGCCTATGGAATATGTCCTCCAGGCTTTGCTCAG 2634
Db 2497 CTCTGGGCCTGCCCCTAAGGGCCTGTGGCCTATGGAATATGTCCTCCAGGCTTTGCTCAG 2556
Qy 2635 CTGAGCTCCTCTTCTGTAAGGAAACCCAGTCATCCCTGAATCTTGCCACAGAGATCCGGG 2694
Db 2557 CTGAGCTCCTCTTCTGTAAGGAAACCCAGTCATCCCTGAATCTTGCCACAGAGATCCGGG 2616
Qy 2695 ATTCAGGAGCTCTCAGTTTCTTAGGGATGGACTATGGCCCAGTCCCCCATCTAAGTGGTG 2754
Db 2617 ATTCAGGAGCTCTCAGTTTCTTAGGGATGGACTATGGCCCAGTCCCCCATCTAAGTGGTG 2676
Qy 2755 CTTTGCAAATGTCTTGGAGGAGTATAGGACAGAGGACCAAAATACACAGCAGGTAGTGTT 2814
Db 2677 CTTTGCAAATGTCTTGGAGGAGTATAGGACAGAGGACCAAAATACACAGCAGGTAGTGTT 2736
Qy 2815 AGCTCTCTGCTAGGAGCTCAAAGCAACACAACTTGTATCAAAATCACAACTGGCAGAGAA 2874
Db 2737 AGCTCTCTGCTAGGAGCTCAAAGCAACACAACTTGTATCAAAATCACAACTGGCAGAGAA 2796
Qy 2875 GCTGGTGGATCCAATCCTTTCTTCATCTGTTGTTATTTAGAACTCACCTCTCACACTCTG 2934
Db 2797 GCTGGTGGATCCAATCCTTTCTTCATCTGTTGTTATTTAGAACTCACCTCTCACACTCTG 2856
Qy 2935 TTCTTTAGTGTCCTTACCTTTATCTTACCACACACATGGGTGTTTCTATTATCCTTGGAA 2994
Db 2857 TTCTTTAGTGTCCTTACCTTTATCTTACCACACACATGGGTGTTTCTATTATCCTTGGAA 2916
Qy 2995 GCACAGACCTCGGGCATCCCCTTATTGCCTGATGGGCCAACACCAACAGTTACGGAGTGC 3054
Db 2917 GCACAGACCTCGGGCATCCCCTTATTGCCTGATGGGCCAACACCAACAGTTACGGAGTGC 2976
Qy 3055 TTGAGAAGGGGCAAGTTTCACAGAAATGGCCAGATAGGGCCTTCCTACAGAGCAGCAAGA 3114
Db 2977 TTGAGAAGGGGCAAGTTTCACAGAAATGGCCAGATAGGGCCTTCCTACAGAGCAGCAAGA 3036
Qy 3115 GTAGGCCAAGCAGAAAGACTGCTGAGGTAACACGGACCCCAGCCCCTGTCAGGGCCTCTG 3174
Db 3037 GTAGGCCAAGCAGAAAGACTGCTGAGGTAACACGGACCCCAGCCCCTGTCAGGGCCTCTG 3096
Qy 3175 CCAAGGAAATAATATGGACCATTTACCTGGCAGGCAGTCTGCTCTCTCTCAGGATCACCA 3234
Db 3097 CCAAGGAAATAATATGGACCATTTACCTGGCAGGCAGTCTGCTCTCTCTCAGGATCACCA 3156
Qy 3235 CGCATCTCAGGATTGGTCTAAACTTCAAGTCTCAACCAAGTGTCTGAAGTGAACTTTGCA 3294
Db 3157 CGCATCTCAGGATTGGTCTAAACTTCAAGTCTCAACCAAGTGTCTGAAGTGAACTTTGCA 3216
Qy 3295 TTGAATAAATTTTTGCCATGGAAAGAACATCAAACAAGCCACTCATCTCTACAGAGATAA 3354
Db 3217 TTGAATAAATTTTTGCCATGGAAAGAACATCAAACAAGCCACTCATCTCTACAGAGATAA 3276
Qy 3355 GAAAACAAGTTTGGCAGAGCAAGAGACAGAAGACCGTGGAGAAATCAGAAGGGGGAACAG 3414
Db 3277 GAAAACAAGTTTGGCAGAGCAAGAGACAGAAGACCGTGGAGAAATCAGAAGGGGGAACAG 3336
Qy 3415 TCAGTTTAGTTAAGGATGGAACCTGGGAAAGGCCACCATTCCTGCTTGATGGGGCTCTGA 3474
Db 3337 TCAGTTTAGTTAAGGATGGAACCTGGGAAAGGCCACCATTCCTGCTTGATGGGGCTCTGA 3396
Qy 3475 TTTGCTCTTGCTCAAGTGGAATAAAACCCCATGGTCTTCTTGACATGATTCTTGATCTTT 3534
Db 3397 TTTGCTCTTGCTCAAGTGGAATAAAACCCCATGGTCTTCTTGACATGATTCTTGATCTTT 3456
Qy 3535 TCTCCACTGAGACACACTTAAGTGATGATCCTTACAGGACTGACACCCTAATGCCAATAA 3594

```
Db   3457 TCTCCACTGAGACACACTTAAGTGATGATCCTTACAGGACTGACACCCTAATGCCAATAA 3516

Qy   3595 AAGTTGCTCATTATGG 3610
          ||||||||||||||||
Db   3517 AAGTTGCTCATTATGG 3532


RESULT 3
ABA96419
ID   ABA96419 standard; cDNA; 2976 BP.
XX
AC   ABA96419;
XX
DT   02-APR-2002  (first entry)
XX
DE   Human 47765 lysyl oxidase encoding cDNA SEQ ID NO 1.
XX
KW   Human; 47765; lysyl oxidase; LSO; cytostatic; haemostatic; hepatotropic;
KW   cardiant; osteopathic; dermatological; antiarteriosclerotic; vasotropic;
KW   antiinflammatory; hypotensive; antiarrhythmic; cell proliferation;
KW   growth; differentiation; leukaemia; tumour; cancer; bone; cartilage;
KW   myeloproliferative; muscular; osteoporosis; cardiovascular; gene therapy;
KW   chromosome mapping; tissue typing; forensic; pharmacogenomic; enzyme;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             95..2365
FT                   /*tag=  a
FT                   /product= "47765 LSO"
XX
PN   WO200192495-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US17405.
XX
PR   26-MAY-2000; 2000US-207650P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyers R;
XX
DR   WPI; 2002-122067/16.
DR   P-PSDB; AAM48743.
XX
PT   Novel human lysyl oxidase polypeptide, designated 47765, and
PT   polynucleotides, useful in the diagnosis and treatment of cell
PT   proliferation disorders, muscular disorders, bone disorders and skin
PT   elasticity disorders  -
XX
PS   Claim 1; Fig 1; 115pp; English.
XX
CC   The invention relates to human lysyl oxidase (LSO) polypeptide,
CC   designated 47765 with cytostatic, haemostatic, hepatotropic, cardiant,
CC   osteopathic, dermatological, antiarteriosclerotic, vasotropic,
CC   antiinflammatory, hypotensive and antiarrhythmic activity. 47765
CC   molecules are useful for identifying a compound which modulates the
CC   activity of the protein, for developing novel diagnostic and therapeutic
CC   agents for LSO-mediated or related disorders including cell
CC   proliferation, growth or differentiation disorder (e.g. carcinoma,
CC   leukaemia, tumour angiogenesis, hepatic disorders and haematopoietic,
CC   myeloproliferative disorders), muscular disorders (e.g. cardiac muscle
CC   disorder, paralysis, ataxia, myotonia and myokymia), bone disorders (e.g.
CC   osteochondrosis and osteoporosis), skin elasticity disorders (e.g. cutis
CC   laxa, Ehlers-Danlos type V syndrome), cardiovascular disorders (e.g.
CC   arteriosclerosis, ischaemia reperfusion injury, restenosis, arterial
CC   inflammation, vascular wall remodeling, tachycardia, vascular heart
CC   disease, long QT syndrome, congestive heart failure, hypertension,
CC   coronary artery disease and arrhythmia) or cartilage based disorders
CC   (e.g. chondromalacia and polychondritis). The encoding polynucleotide is
CC   useful in chromosome mapping, tissue typing, forensic identification, as
CC   markers for pharmacogenomic profiling of a subject and in gene therapy.
XX
SQ   Sequence 2976 BP; 620 A; 850 C; 909 G; 584 T; 13 other;

  Query Match             78.7%;  Score 2844.4;  DB 24;  Length 2976;
  Best Local Similarity   97.6%;  Pred. No. 0;
  Matches 2872;  Conservative   11;  Mismatches   59;  Indels    0;  Gaps    0;

Qy      60 CAAGCCCCCTCTTTCCTAGCCTGGACAGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 119
           ||  |||   || |||  ||      | ||||||||||||||||||||||||||||||||||||
Db      35 CAGCCCCGGACTGTCCGCGCTCCATCTGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 94

Qy     120 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      95 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 154

Qy     180 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 239
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     155 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 214

Qy     240 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 299
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     215 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 274

Qy     300 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 359
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     275 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 334

Qy     360 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 419
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     335 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 394

Qy     420 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 479
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     395 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 454

Qy     480 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCGGCGCCATCGTGGCTAC 539
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     455 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCGGCGCCATCGTGGCTAC 514

Qy     540 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGG 599
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     515 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGG 574

Qy     600 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 659
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     575 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 634

Qy     660 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCACGGCTGGACCATGAACAACAGC 719
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     635 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCACGGCTGGACCATGAACAACAGC 694

Qy     720 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTCCCTGTCGACAGCCACTACTAC 779
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     695 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTCCCTGTCGACAGCCACTACTAC 754

Qy     780 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCCAGGCTGAAGAGCCTGACGAAT 839
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Qy     840 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGCACAGAGCCCCACATGGCCAAC 899
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Qy     900 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 959
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Qy     960 CATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGTCCACCGAAGACAAAGCCACAA 1019
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Db     935 CACGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGTCCACCGAAGACAAAGCCACAA 994

Qy    1020 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTTCGCTCCGGGGCCCAGGTGGGC 1079
```

RESULT 4
AAD33480
ID AAD33480 standard; cDNA; 2603 BP.
XX
AC AAD33480;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human drug metabolising enzyme (DME-1) cDNA.
XX

KW Human; drug metabolising enzyme; cell proliferative disorder; metabolic;
KW autoimmune; inflammatory; developmental; gastrointestinal; hypergonadal;
KW pancreatic; endocrine; eye; dermatitis; Addison's disease; antilipaemic;
KW acquired immunodeficiency syndrome; AIDS; glomerulonephritis; anorectic;
KW diabetes; atherosclerosis; adult respiratory distress syndrome; anaemia;
KW Grave's disease; thyroiditis; Crohn's disease; infection; anticoagulant;
KW systemic lupus erythematosus; cirrhosis; psoriasis; epilepsy; gastritis;
KW cataract; hypopituitarism; cancer; rheumatoid arthritis; conjunctivitis;
KW cystic fibrosis; peptic ulcer; Wilson's disease; hepatitis; antithyroid;
KW allergy; diarrhoea; thrombosis; obesity; immunostimulant; tranquillizer;
KW infertility; vulnerary; anticonvulsant; gynaecological; laxative; goitre;
KW nootropic; jaundice; trauma; asthma; DME-1; enzyme; gene; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..2271
FT		/*tag= a
FT		/product= "Human DME-1"
FT	sig_peptide	1..72
FT		/*tag= b
FT	mat_peptide	73..2268
FT		/*tag= c
FT		/product= "Mature human DME-1 protein"

XX
PN WO200212467-A2.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001WO-US24382.
XX
PR 04-AUG-2000; 2000US-223055P.
PR 11-AUG-2000; 2000US-224728P.
PR 18-AUG-2000; 2000US-226440P.
PR 24-AUG-2000; 2000US-228067P.
PR 31-AUG-2000; 2000US-230063P.
PR 13-SEP-2000; 2000US-232244P.
PR 20-SEP-2000; 2000US-234269P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Baughn MR, Bruns CM, Das D, Delegeane AM, Ding L, Elliot VS;
PI Gandhi AR, Griffin JA, Hafalia AJA, Khan FA, Lal P, Lee S;
PI Lu DAM, Lu Y, Patterson C, Ramkumar J, Ring HZ, Sanjanwala MS;
PI Tang YT, Thangavelu K, Thornton M, Tribouley CM, Walia NK;
PI Warren BA, Yang J, Yao MG, Yue H;
XX
DR WPI; 2002-206331/26.
DR P-PSDB; AAE21043.
XX
PT New human drug metabolizing enzyme polypeptide and polynucleotide
PT useful for diagnosing, treating and preventing cell proliferative,
PT autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
PT disorders
XX
PS Claim 64; Page 166; 179pp; English.
XX
CC The invention relates to an isolated human drug metabolising enzyme (DME)
CC polypeptide or a biologically active or immunogenic fragment of DME. DME
CC is useful for diagnosis, treatment and prevention of cell proliferative,
CC autoimmune/inflammatory, developmental, endocrine, eye, metabolic and
CC gastrointestinal disorders including live disorders. Autoimmune/
CC inflammatory disorders include acquired immunodeficiency syndrome (AIDS),
CC adult respiratory distress syndrome, Addison's disease, atherosclerosis,
CC allergies, anaemia, asthma, autoimmune haemolytic anaemia, autoimmune
CC thyroiditis, Crohn's disease, atopic dermatitis, diabetes mellitus,
CC glomerulonephritis, rheumatoid arthritis, systemic lupus erythematosus,
CC ulcerative colitis, uveitis, viral, bacterial, protozoal, parasitic,
CC fungal, helminthic infections and trauma. Cell proliferative disorders
CC include cancer, arteriosclerosis, cirrhosis and psoriasis; developmental
CC disorders include epilepsy and cataract; and endocrine disorders include
CC disorders of hypothalamus/pituitary, disorders associated with
CC hypopituitarism, including diabetes insipidus, hypogonadism, disorders
CC associated with hypothyroidism including goitre, Grave's disease,
CC pancreatic disorders such as diabetes mellitus, disorders associated with
CC adrenals, disorders associated with gonadal steroid hormones such as
CC endometriosis, infertility, hypergonadal disorders and gynaecomastia.
CC Disorders of the eye include conjunctivitis and macular degeneration and
CC metabolic disorders include diabetes, cystic fibrosis, obesity and
CC hypocalcaemia. Gastrointestinal disorders include gastritis, peptic
CC ulcer, hepatitis, constipation, diarrhoea, jaundice, Wilson's disease,
CC thrombosis and hepatic tumours. DME gene is useful in gene therapy. The
CC present sequence is human DME-1 cDNA.
XX
SQ Sequence 2603 BP; 532 A; 753 C; 827 G; 491 T, 0 other;

Query Match 71.8%; Score 2597.2; DB 24; Length 2603;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy   120 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 179
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Db     1 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT  60

Qy   180 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 239
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    61 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 120

Qy   240 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 299
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Db   121 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 180

Qy   300 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 240

Qy   360 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 300

Qy   420 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 360

Qy   480 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 420

Qy   540 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGG 599
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Db   421 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCAGCGGCTGGAGGAGGTGCGG 480

Qy   600 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 659
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Db   481 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 540

Qy   660 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCACGGCTGGACCATGAACAACAGC 719
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Db   541 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCACGGCTGGACCATGAACAACAGC 600

Qy   720 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 779
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Db   601 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 660

Qy   780 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCCAGGCTGAAGAGCCTGACGAAT 839
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Qy   840 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 780

Qy   900 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 959
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Db   781 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 840
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Qy    960 CATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAA 1019
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Db    841 CATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAA 900

Qy   1020 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGC 1079
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Db    901 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGC 960

Qy   1080 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1139
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Db    961 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1020

Qy   1140 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1199
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Db   1021 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1080

Qy   1200 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGC 1259
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Db   1081 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGC 1140

Qy   1260 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1319
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Db   1141 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1200

Qy   1320 CAACATGAGAATGCTGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGAATCAG 1379
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Qy   1440 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1499
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Db   1321 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1380

Qy   1500 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCTGGTTC 1559
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Qy   1560 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1619
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Qy   1620 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1679
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Db   1501 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1560

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Db   1681 GAGGAGAACTGCCTCTCCAAGTCTGCGGATCACATGGACTGGCCCTACGGATACCGCCGC 1740

Qy   1860 CTATTGCGCTTCTCCACACAGATCTACAATCTGGGCCGGACTGACTTTCGTCCAAAGACT 1919
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Db   1741 CTATTGCGCTTCTCCACACAGATCTACAATCTGGGCCGGACTGACTTTCGTCCAAAGACT 1800

Qy   1920 GGACGCGATAGCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGGTCTTC 1979
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Qy   2040 TTCTGTCTGGAGGACACAAACTGCCCCACAGGACTGCAGCGGCGCTACGCATGTGCCAAC 2099
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Qy   2280 TATGATGGGCACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATACCCAGCCAAT 2339
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Db   2161 TATGATGGGCACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATACCCAGCCAAT 2220

Qy   2340 GCAGAACTCTCCCTGGAGCAGGAACAGCGTCTCAGGAACAACCTCATCTGAAGCTGTCAC 2399
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Db   2221 GCAGAACTCTCCCTGGAGCAGGAACAGCGTCTCAGGAACAACCTCATCTGAAGCTGTCAC 2280

Qy   2400 TGCACACTCCTAGCTGCTGCCGATACACCAGATACCTCAGCTTATTGGAGCCATGCCCTT 2459
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Db   2281 TGCACACTCCTAGCTGCTGCCGATACACCAGATACCTCAGCTTATTGGAGCCATGCCCTT 2340

Qy   2460 CACAGAGTCCCAACTCAGAGGAAAAGGGCCAGTGCCAAGGGGCACCAAGAACCTGCTCAG 2519
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Qy   2520 GAAGCCTTTTGATGGCAAGATCACCAATCCAGATGGTATTGCTCCCTCAGGATGGCTCTG 2579
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Qy   2580 GGCCTGCCCCTAAGGGCCTGTGGCCTATGGAATATGTCCTCCAGGCTTTGCTCAGCTGAG 2639
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Db   2521 CTCCTCTTCTGTAAGGAAACCCAGTCATCCCTGAATCTTGCCACAGAGATCCGGGATTCA 2580

Qy   2700 GGAGCTCTCAGTTTCTTAGGGA 2721
          |||||||||||||||||| |||
Db   2581 GGAGCTCTCAGTTTCTTAAGGA 2602
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RESULT 5
ABA96420
ID ABA96420 standard; cDNA; 2268 BP.
XX
AC ABA96420;
XX
DT 02-APR-2002 (first entry)
XX
DE Human 47765 lysyl oxidase coding sequence SEQ ID NO 3.
XX
KW Human; 47765; lysyl oxidase; LSO; cytostatic; haemostatic; hepatotropic;
KW cardiant; osteopathic; dermatological; antiarteriosclerotic; vasotropic;
KW antiinflammatory; hypotensive; antiarrhythmic; cell proliferation;
KW growth; differentiation; leukaemia; tumour; cancer; bone; cartilage;
KW myeloproliferative; muscular; osteoporosis; cardiovascular; gene therapy;
KW chromosome mapping; tissue typing; forensic; pharmacogenomic; enzyme;
KW gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..2268
FT   /*tag= a
FT   /product= "47765 LSO"
FT   /partial

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FT                   /note= "the CDS lacks a stop codon"
XX
PN   WO200192495-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US17405.
XX
PR   26-MAY-2000; 2000US-207650P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyers R;
XX
DR   WPI; 2002-122067/16.
DR   P-PSDB; AAM48743.
XX
PT   Novel human lysyl oxidase polypeptide, designated 47765, and
PT   polynucleotides, useful in the diagnosis and treatment of cell
PT   proliferation disorders, muscular disorders, bone disorders and skin
PT   elasticity disorders -
XX
PS   Claim 1; Fig 1; 115pp; English.
XX
CC   The invention relates to human lysyl oxidase (LSO) polypeptide,
CC   designated 47765 with cytostatic, haemostatic, hepatotropic, cardiant,
CC   osteopathic, dermatological, antiarteriosclerotic, vasotropic,
CC   antiinflammatory, hypotensive and antiarrhythmic activity. 47765
CC   molecules are useful for identifying a compound which modulates the
CC   activity of the protein, for developing novel diagnostic and therapeutic
CC   agents for LSO-mediated or related disorders including cell
CC   proliferation, growth or differentiation disorder (e.g. carcinoma,
CC   leukaemia, tumour angiogenesis, hepatic disorders and haematopoietic,
CC   myeloproliferative disorders), muscular disorders (e.g. cardiac muscle
CC   disorder, paralysis, ataxia, myotonia and myokymia), bone disorders (e.g.
CC   osteochondrosis and osteoporosis), skin elasticity disorders (e.g. cutis
CC   laxa, Ehlers-Danlos type V syndrome), cardiovascular disorders (e.g.
CC   arteriosclerosis, ischaemia reperfusion injury, restenosis, arterial
CC   inflammation, vascular wall remodeling, tachycardia, vascular heart
CC   disease, long QT syndrome, congestive heart failure, hypertension,
CC   coronary artery disease and arrhythmia) or cartilage based disorders
CC   (e.g. chondromalacia and polychondritis). The encoding polynucleotide is
CC   useful in chromosome mapping, tissue typing, forensic identification, as
CC   markers for pharmacogenomic profiling of a subject and in gene therapy.
XX
SQ   Sequence 2268 BP; 453 A; 656 C; 745 G; 414 T; 0 other;
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Query Match 62.6%; Score 2263.2; DB 24; Length 2268;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2265; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy     120 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 179
Db       1 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT  60

Qy     180 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 239
Db      61 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 120

Qy     240 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 299
Db     121 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 180

Qy     300 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 359
Db     181 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 240

Qy     360 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 419
Db     241 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 300

Qy     420 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 479
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Db     301 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGT?TAATGGCTGGGGAGTCAGT 360

Qy     480 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACC?CCGGCGCCATCGTGGCTAC 539
Db     361 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACC?CCGGCGCCATCGTGGCTAC 420

Qy     540 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCC?GCGGCTGGAGGAGGTGCGG 599
Db     421 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCC?GCGGCTGGAGGAGGTGCGG 480

Qy     600 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCACTGACCGAGGGAGCCGTGGAG 659
Db     481 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAC?GACCGAGGGAGCCGTGGAG 540

Qy     660 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGC GCTGGACCATGAACAACAGC 719
Db     541 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGC GCTGGACCATGAACAACAGC 600

Qy     720 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTG?CTGTCGACAGCCACTACTAC 779
Db     601 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTG?CTGTCGACAGCCACTACTAC 660

Qy     780 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCT?GGCTGAAGAGCCTGACGAAT 839
Db     661 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCT?GGCTGAAGAGCCTGACGAAT 720

Qy     840 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGG?CAGAGCCCCACATGGCCAAC 899
Db     721 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGG?CAGAGCCCCACATGGCCAAC 780

Qy     900 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGG?CAGCCTGCCCAGGTGGCATG 959
Db     781 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGG?CAGCCTGCCCAGGTGGCATG 840

Qy     960 CATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGC?CCACCGAAGACAAAGCCACAA 1019
Db     841 CACGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGC?CCACCGAAGACAAAGCCACAA 900

Qy    1020 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTC?CGCTCCGGGGCCCAGGTGGGC 1079
Db     901 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTC?CGCTCCGGGGCCCAGGTGGGC 960

Qy    1080 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGC?ACGGTCTGTGACCACAGGTGG 1139
Db     961 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGC?ACGGTCTGTGACCACAGGTGG 1020

Qy    1140 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGC?TTTGGCTCTGCTCGGGAGGCC 1199
Db    1021 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGC?TTTGGCTCTGCTCGGGAGGCC 1080

Qy    1200 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCAT?CCACCTGAGTGAGGTGCGCTGC 1259
Db    1081 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCAT?CCACCTGAGTGAGGTGCGCTGC 1140

Qy    1260 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCT?GGAAGGGTCCCAGAATGGTTGC 1319
Db    1141 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCT?GGAAGGGTCCCAGAATGGTTGC 1200

Qy    1320 CAACATGAGAATGCTGCTGCTGTCAGGTGCAATGTCCC?AACATGGGCTTTCAGAATCAG 1379
Db    1201 CAACATGAGAATGATGCTGCTGTCAGGTGCAATGTCCC?AACATGGGCTTTCAGAATCAG 1260

Qy    1380 GTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCT?ATTGGAGGTGCAGGTGGAGGTG 1439
Db    1261 GTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCT?ATTGGAGGTGCAGGTGGAGGTG 1320

Qy    1440 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAA?CTGGGGGCTCACCGAAGCCATG 1499
Db    1321 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAA?CTGGGGGCTCACCGAAGCCATG 1380

Qy    1500 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCC?TGCCTACAAGGAAACCTGGTTC 1559
Db    1381 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCC?TGCCTACAAGGAAACCTGGTTC 1440
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Qy   1560 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1500

Qy   1620 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1560

Qy   1680 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1620

Qy   1740 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1680

Qy   1800 GAGGAGAACTGCCTCTCCAAGTCTGCGGATCACATGGACTGGCCCTACGGATACCGCCGC 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GAGGAGAACTGCCTCTCCAAGTCTGCAGATCACATGGACTGGCCCTACGGATACCGCCGC 1740

Qy   1860 CTATTGCGCTTCTCCACACAGATCTACAATCTGGGCCGGACTGACTTTCGTCCAAAGACT 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTATTGCGCTTCTCCACACAGATCTACAATCTGGGCCGGACTGACTTTCGTCCAAAGACT 1800

Qy   1920 GGACGCGATAGCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGGTCTTC 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GGACGCGATAGCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGGTCTTC 1860

Qy   1980 ACCCACTACGACCTCCTCACTCTCAATGGCTCCAAGGTGGCTGAGGGGCACAAGGCCAGC 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 ACCCACTACGACCTCCTCACTCTCAATGGCTCCAAGGTGGCTGAGGGGCACAAGGCCAGC 1920

Qy   2040 TTCTGTCTGGAGGACACAAACTGCCCCACAGGACTGCAGCGGCGCTACGCATGTGCCAAC 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TTCTGTCTGGAGGACACAAACTGCCCCACAGGACTGCAGCGGCGCTACGCATGTGCCAAC 1980

Qy   2100 TTTGGAGAACAGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACATTGATTGC 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TTTGGAGAACAGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACATTGATTGC 2040

Qy   2160 CAGTGGGTGGATATCACAGATGTGGGCCCCGGGAATTATATCTTCCAGGTGATTGTGAAC 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGTGGGTGGATATCACAGATGTGGGCCCCGGGAATTATATCTTCCAGGTGATTGTGAAC 2100

Qy   2220 CCCCACTATGAAGTGGCAGAGTCAGATTTCTCCAACAATATGCTGCAGTGCCGCTGCAAG 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCCCACTATGAAGTGGCAGAGTCAGATTTCTCCAACAATATGCTGCAGTGCCGCTGCAAG 2160

Qy   2280 TATGATGGGCACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATACCCAGCCAAT 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TATGATGGGCACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATACCCAGCCAAT 2220

Qy   2340 GCAGAACTCTCCCTGGAGCAGGAACAGCGTCTCAGGAACAACCTCATC 2387
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GCAGAACTCTCCCTGGAGCAGGAACAGCGTCTCAGGAACAACCTCATC 2268
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RESULT 6
AAA96737
ID AAA96737 standard; DNA; 3767 BP.
XX
AC AAA96737;
XX
DT 19-FEB-2001 (first entry)
XX
DE Polynucleotide isolated from lymph node stromal cells of fsn -/- mice.
XX
KW Lymph node stromal cell; fsn -/- mice; inflammatory disorder;
KW immune system disorder; cancer; viral disorder; HIV infection;
KW blood vessel growth; tumour necrosis factor disorder; arthritis;
KW inflammatory bowel disease; fibroblast growth factor-mediated disorder;
KW cardiac failure; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 129..2402
FT /*tag= a
XX
PN WO200058463-A1.
XX
PD 05-OCT-2000.
XX
PF 18-FEB-2000; 2000WO-NZ00015.
XX
PR 25-MAR-1999; 99US-0276268.
PR 26-AUG-1999; 99US-0383586.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD;
PI Murison JG;
XX
DR WPI; 2000-664924/64.
DR P-PSDB; AAB19127.
XX
PT Polypeptide expressed in mammalian fsn -/- lymph node stromal cells,
PT useful for modulating growth of blood cells, for treating inflammatory
PT and tumour necrosis factor-mediated disorders, cancer and viral
PT disorders -
XX
PS Claim 4; Page 61-63; 75pp; English.
XX
CC The present sequence represents a polynucleotide sequence which is
CC isolated from lymph node stromal cells of fsn -/- mice. The
CC polynucleotides and their polypeptides are useful for treating an
CC inflammatory disorder, disorder of immune system and cancer selected
CC from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a
CC viral disorder, in particular HIV infection and for modulating the
CC growth of blood vessels. The polypeptides are useful for treating a
CC tumour necrosis factor (TNF) mediated disorder, such as those selected
CC from arthritis, inflammatory bowel disease and cardiac failure and a
CC fibroblast growth factor-mediated disorder. It is also useful in assays
CC to determine biological activity, to raise antibodies, to isolate
CC corresponding ligands or receptors, to quantify levels of protein or
CC cognate corresponding ligand or receptors, as antiinflammatory agents,
CC and in compositions for the treatment of skin, connective tissue and
CC immune system diseases. The polynucleotide is useful as marker for
CC tissue, as a chromosome marker or tags in the identification of a
CC genetic disorder.
XX
SQ Sequence 3767 BP; 877 A; 1047 C; 1080 G; 763 T; 0 other;

Query Match 53.1%; Score 1918.8; DB 21; Length 3767;
Best Local Similarity 77.0%; Pred. No. 0;
Matches 2709; Conservative 0; Mismatches 652; Indels 159; Gaps 24;

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Qy    110 TGAAGTCACCATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTG---CTGCTGCT 166
          |||| ||||||||  |||| ||| |||| ||||| |||  |||||||||   ||||||||
Db    119 TGAAATCACCATGATGTGGCCCCAACCACCCACCTTCTCCCTGTTCCTGCTACTGCTGCT 178

Qy    167 AGGCCAGCCCCCTCCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGG 226
          | ||||  ||||| |||| ||||||||||||   |||||||  |||||| |||| |||||
Db    179 AAGCCAAGCCCCTTCCAGTAGGCCACAGTCATCAGGCACCAAGAAGCTCAGGCTTGTGGG 238

Qy    227 CCCAGAGAGCAAGCCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCAC 286
          |||| |  ||  ||| ||||||||||| ||||||||||||||||||||||||||||||||
Db    239 GCCAGCGGACAGACCAAAGGAGGGCCGCTTGGAGGTGCTGCACCAGGGCCAGTGGGGCAC 298

Qy    287 CGTGTGTGATGACAACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTT 346
          |||||||||||  | || ||| |||||||||| || ||||| ||||| ||||||||||
Db    299 GGTGTGTGATGATGATTTCGCTCTCCAGGAGGCTACTGTGGCCTGCCGACAGCTGGGCTT 358

Qy    347 CGAAGCTGCCTTGACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTG 406
          ||  | ||||||||||||||| |||||||||||||| || ||||| ||||| ||||||||
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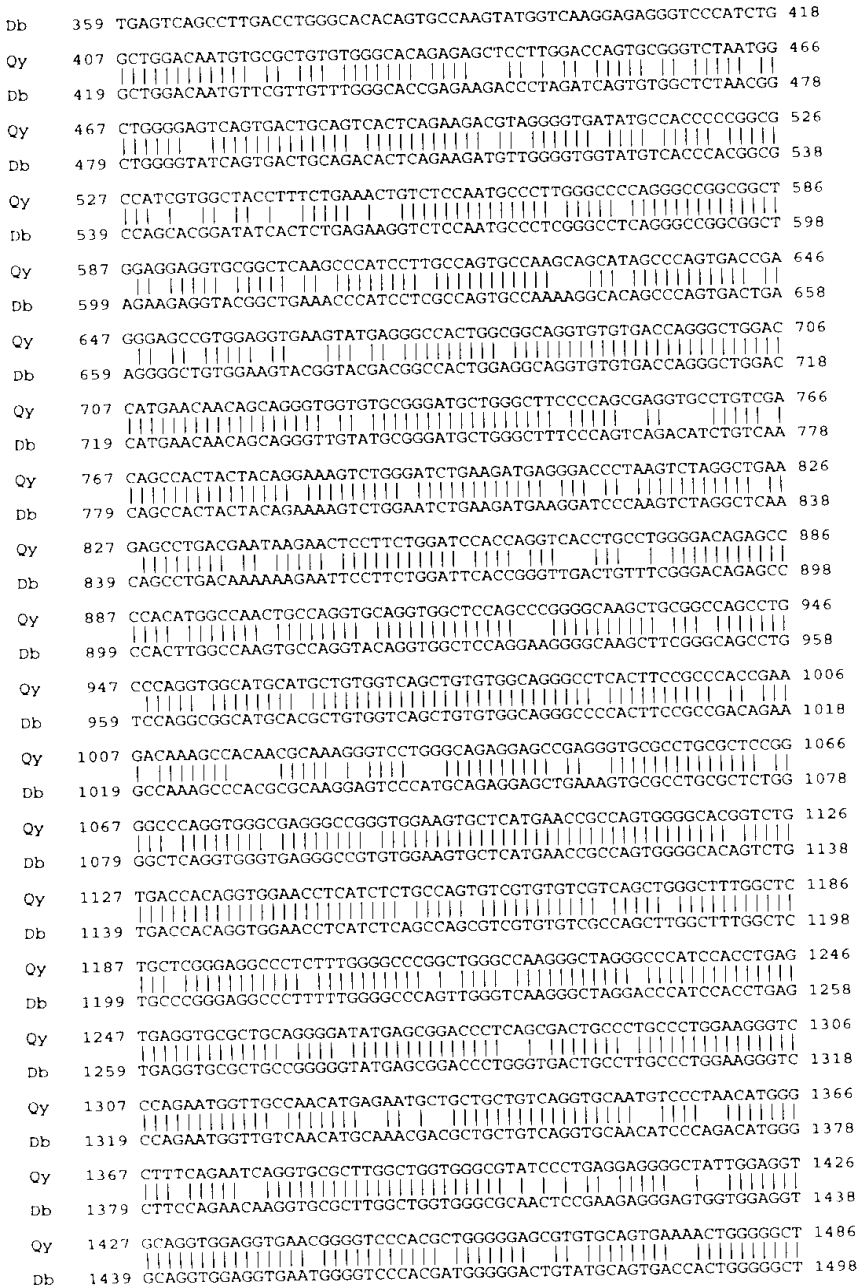
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Qy 407 GCTGGACAATGTGCGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGG 466
Db 419 GCTGGACAATGTTCGTTGTTTGGGCACCGAGAAGACCCTAGATCAGTGTGGCTCTAACGG 478
Qy 467 CTGGGGAGTCAGTGACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCG 526
Db 479 CTGGGGTATCAGTGACTGCAGACACTCAGAAGATGTTGGGGTGGTATGTCACCCACGGCG 538
Qy 527 CCATCGTGGCTACCTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCGGCGGCT 586
Db 539 CCAGCACGGATATCACTCTGAGAAGGTCTCCAATGCCCTCGGGCCTCAGGGCCGGCGGCT 598
Qy 587 GGAGGAGGTGCGGCTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGA 646
Db 599 AGAAGAGGTACGGCTGAAACCCATCCTCGCCAGTGCCAAAAGGCACAGCCCAGTGACTGA 658
Qy 647 GGGAGCCGTGGAGGTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGAC 706
Db 659 AGGGGCTGTGGAAGTACGGTACGACGGCCACTGGAGGCAGGTGTGTGACCAGGGCTGGAC 718
Qy 707 CATGAACAACAGCAGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGA 766
Db 719 CATGAACAACAGCAGGGTTGTATGCGGGATGCTGGGCTTTCCCAGTCAGACATCTGTCAA 778
Qy 767 CAGCCACTACTACAGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAA 826
Db 779 CAGCCACTACTACAGAAAAGTCTGGAATCTGAAGATGAAGGATCCCAAGTCTAGGCTCAA 838
Qy 827 GAGCCTGACGAATAAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCC 886
Db 839 CAGCCTGACAAAAAAGAATTCCTTCTGGATTCACCGGGTTGACTGTTTCGGGACAGAGCC 898
Qy 887 CCACATGGCCAACTGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTG 946
Db 899 CCACTTGGCCAAGTGCCAGGTACAGGTGGCTCCAGGAAGGGGCAAGCTTCGGGCAGCCTG 958
Qy 947 CCCAGGTGGCATGCATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAA 1006
Db 959 TCCAGGCGGCATGCACGCTGTGGTCAGCTGTGTGGCAGGGCCCCACTTCCGCCGACAGAA 1018
Qy 1007 GACAAAGCCACAACGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGG 1066
Db 1019 GCCAAAGCCCACGCGCAAGGAGTCCCATGCAGAGGAGCTGAAAGTGCGCCTGCGCTCTGG 1078
Qy 1067 GGCCCAGGTGGGCGAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTG 1126
Db 1079 GGCTCAGGTGGGTGAGGGCCGTGTGGAAGTGCTCATGAACCGCCAGTGGGGCACAGTCTG 1138
Qy 1127 TGACCACAGGTGGAACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTC 1186
Db 1139 TGACCACAGGTGGAACCTCATCTCAGCCAGCGTCGTGTGTCGCCAGCTTGGCTTTGGCTC 1198
Qy 1187 TGCTCGGGAGGCCCTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAG 1246
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Qy 1247 TGAGGTGCGCTGCAGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTC 1306
Db 1259 TGAGGTGCGCTGCCGGGGGTATGAGCGGACCCTGGGTGACTGCCTTGCCCTGGAAGGGTC 1318
Qy 1307 CCAGAATGGTTGCCAACATGAGAATGCTGCTGCTGTCAGGTGCAATGTCCCTAACATGGG 1366
Db 1319 CCAGAATGGTTGTCAACATGCAAACGACGCTGCTGTCAGGTGCAACATCCCAGACATGGG 1378
Qy 1367 CTTTCAGAATCAGGTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCTATTGGAGGT 1426
Db 1379 CTTCCAGAACAAGGTGCGCTTGGCTGGTGGGCGCAACTCCGAAGAGGGAGTGGTGGAGGT 1438
Qy 1427 GCAGGTGGAGGTGAACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCT 1486
Db 1439 GCAGGTGGAGGTGAATGGGGTCCCACGATGGGGGACTGTATGCAGTGACCACTGGGGGCT 1498
Qy 1487 CACCGAAGCCATGGTGGCCTGCCGACAGCTCGGCCTGGGT TTGCCATCCATGCCTACAA 1546
Db 1499 CACCGAAGCCATGGTGACCTGTCGGCAACTTGGTCTGGGA TTGCCAACTTTGCTCTCAA 1558
Qy 1547 GGAAACCTGGTTCTGGTCGGGGACGCCAAGGGCCCAGGAG TGGTGATGAGTGGGGTGCG 1606
Db 1559 GGACACCTGGTACTGGCAGGGGACACCAGAGGCCAAAGAA TGGTGATGAGTGGAGTTCG 1618
Qy 1607 CTGCTCAGGCACAGAGCTGGCCCTGCAGCAGTGCCAGAGG CACGGGCCGGTGCACTGCTC 1666
Db 1619 CTGCTCCGGCACAGAAATGGCCCTGCAGCAGTGTCAGAGC CATGGGCCGGTGCACTGTTC 1678
Qy 1667 CCACGGTGGCGGGCGCTTCCTGGCTGGAGTCTCCTGCATC GACAGTGCACCAGACCTGGT 1726
Db 1679 CCACGGCCCAGGGCGCTTCTCGGCTGGCGTTGCTTGTATC AACAGTGCTCCAGACCTCGT 1738
Qy 1727 GATGAACGCCCAGCTAGTGCAGGAGACGGCCTACTTGGAC GACCGCCCGCTCAGCCAGCT 1786
Db 1739 GATGAACGCCCAGCTGGTACAAGAGACGGCGTACTTGGAC GATCGTCCACTCAGCATGCT 1798
Qy 1787 GTATTGTGCCCACGAGGAGAACTGCCTCTCCAAGTCTGCG GATCACATGGACTGGCCCTA 1846
Db 1799 GTACTGTGCTCACGAGGAAAACTGCCTCTCCAAGTCCGC GATCACATGGACTGGCCCTA 1858
Qy 1847 CGGATACCGCCGCCTATTGCGCTTCTCCACACAGATCTA CAATCTGGGCCGGACTGACTT 1906
Db 1859 CGGGTACCGGCGCTTGCTGCGCTTCTCCTCACAGATCTA CAACCTTGGCCGGGCCGACTT 1918
Qy 1907 TCGTCCAAAGACTGGACGCGATAGCTGGGTTTGGCACCA GTGCCACAGGCATTACCACAG 1966
Db 1919 CCGTCCCAAGGCTGGACGCCACAGCTGGATTTGGCACCA GTGCCACAGGCACTACCACAG 1978
Qy 1967 CATTGAGGTCTTCACCCACTACGACCTCCTCACTCTCAA TGGCTCCAAGGTGGCTGAGGG 2026
Db 1979 CATCGAAGTCTTCACTCATTATGACCTGCTCACGCTCAA TGGCTCCAAGGTGGCCGAGGG 2038
Qy 2027 GCACAAGGCCAGCTTCTGTCTGGAGGACACAAACTGCCCC ACAGGACTGCAGCGGCGCTA 2086
Db 2039 ACACAAGGCCAGCTTCTGTCTAGAAGATACAAACTGCCCC TCAGGAGTGCAGCGGCGCTA 2098
Qy 2087 CGCATGTGCCAACTTTGGAGAACAGGGAGTGACTGTAGCC TGCTGGGACACCTACCGGCA 2146
Db 2099 TGCATGTGCCAACTTTGGGGAACAGGGAGTGGCTGTAGC CTGCTGGGACACCTACCGGCA 2158
Qy 2147 TGACATTGATTGCCAGTGGGTGGATATCACAGATGTGGC CCCCGGGAATTATATCTTCCA 2206
Db 2159 TGACATCGATTGCCAGTGGGTGGATATCACAGATGTGGC TCCAGGGGACTATATCTTCCA 2218
Qy 2207 GGTGATTGTGAACCCCCACTATGAAGTGGCAGAGTCAGA TTTCTCCAACAATATGCTGCA 2266
Db 2219 GGTGGTTGTGAACCCCACAAACGATGTTGCAGAGTCCGA TTTCTCCAATAACATGATACG 2278
Qy 2267 GTGCCGCTGCAAGTATGATGGGCACCGGGTCTGGCTGCA CAACTGCCACACAGGGAATTC 2326
Db 2279 GTGCCGCTGCAAGTATGATGGACAGCGAGTCTGGTTGCA CAACTGCCACACAGGAGATTC 2338
Qy 2327 ATACCCAGCCAATGCAGAACTCTCCCTGGAGCAGGAACAG CGTCTCAGGAACAACCTCAT 2386
Db 2339 CTACCGAGCCAATGCAGAGCTCTCCCTGGAGCAGGAACAG CGACTCAGGAACAACTTGAT 2398
Qy 2387 CTGAAGCTGTCACTGCACACTCCTAGCTGCTGCCGATA CACCAGATACCTCAGCTTATTG 2446
Db 2399 CTGAAGCCATTACTGCACTCCCAGCTCTGCT---CACA CACCAGATACCTCAGCTGACTG 2455
Qy 2447 GAGCCATGCCCTTCACAGAGTCCCAACTCAGAGGA-AA AGGGCCAGTGCCAAGGGGCACC 2505
Db 2456 GAGCCATGCCCTTCACAAAGCCCTGACTCACAGGACAA AGGGCTAGTGACAAGGAGCACC 2515
Qy 2506 AAGAACCTGCTCAGGAAGCCTTTTGATGGCAAGATCACC AATCCAGATGGTATTGCTCCC 2565
Db 2516 AAGAAGCTGCTCAGGAGGCCTTTCAGTGGCCAGATCAT CACCCGGGATGGCA--GTTCTC 2573

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Qy   2566 TCAGGATGGCTCTGGGCCTGCCCCTAAGGGCCTGTGGCCTATGGAATATGTCCTCCAGGC 2625
          ||||||||||||||||||| || |
Db   2574 TCAGGATGGCTCTGGGCCAGCTC---------------------------------------- 2596

Qy   2626 TTTGCTCAGCTGAGCTCCTCTTCTGTAAGGAAACCCAGTCATCCCTGAATCTTGCCACAG 2685
                    | || ||||||  | |||| || |  || ||  |  | ||||   ||
Db   2597 -----------AACCTTCTCTTCCTTCAGGAGACTCGATCTTCTTTACAACTTGATGCAC 2645

Qy   2686 AGATCCGGGATTCAGGAGCTCTCAGTTTCTTAGGGATGGACTATGGCCCAGTCCCCCATC 2745
          || |||  | ||||||||||| |||| || |||||| ||| || || || ||||| ||
Db   2646 AGTTCCCAGTTTCAGGAGCTCTAAGTTCCTCAGGGATGAACTGTGACCAAGGCCCCC-TC 2704

Qy   2746 TAAGTGGTGCTTTGCAAATGTCTTGGAGGAGTATAGGACAGAGGACCAAAATACACAGCA 2805
          ||||||||||||||||||||||||||||  | |||||||| ||||  |  |||||
Db   2705 TAAGTGGTGCTTTGCAAATGTCTTGGAGGACCAAAGGACAGACGACCCGAGAACACAAGC 2764

Qy   2806 GGTAGTGTTAG-----CTCTCTGCTAGGAGCTCAAAGCAACACAACTTGTATCAAAATCA 2860
            || |   ||      |||||||||   |||| | |||| |  ||   | ||||| |||
Db   2765 TGTGGATGGAGTCGTTTTCTCTGCTATACGCTCCACGCAAAAGGAC-CATGTCAAAGTCA 2823

Qy   2861 CAACTGGCAGAGAAGCTGGTGGATCCAATCCTTTCTTCATCTGTTGTTATTTAGAACTCA 2920
          || |||||||||| ||||||| |  || |||   ||      |    | | |||||||||
Db   2824 CACCTGGCAGAGACGCTGGTGAACACAGTCC---CTCAGCTTACCCTCACTTAGAACTCG 2880

Qy   2921 CCTCTCACACTCTG-----TTCTTTAGTGTCCTTACCTTTATCTTACCACACACATGGGT 2975
          | |||||  |||||     |    | |  || ||||||| ||      ||||||    |||
Db   2881 CATCTCAGGCTCTGAAGCCTCTCCTTGCATCTTTACCTTCATTCGGTCACACA---TGGT 2937

Qy   2976 GTTTCTATTATCCTTGGAAGCACAGACCTCGGGCATCCCCTTATTGCCTGATGGGCCAAC 3035
          ||||| | ||||| || |  | ||| |||          ||   ||| |||||||||| ||||
Db   2938 GTTTCCAATATCCCTGAACCCTCAGGCCT--------CCTCCATTTCCTGATGGGTCAAC 2989

Qy   3036 ACCAACAGTTACGGAGTGCTTGAGAAGGGGCAAGTTTCACAGAAATGGCCAGATAGGGCC 3095
          |||   | |   ||          |    || ||||||||||||||           || |
Db   2990 ACCTCGATTATTGG------GGCTGGGGAGCAAGTTTCACAGAATGACGAGACAGGGCCT 3043

Qy   3096 TTCCTACAGAGCAGCAAGAGTAGGCCAAGCAGAAAGACTGCTGAGGTAACACGGACCCCA 3155
          ||||| ||||| ||  |||       |||||  | ||  |||||||| ||| | |  |
Db   3044 TTCCTGCAGAGTAGTCAGA-------AAGCAAGACGAAGGCTGAGGTCACATGAATTC-- 3094

Qy   3156 GCCCCTGTCAGGGCCTCTGCCAAGGAAATAATATGGACCATTTACCTGGCAGGCAGTCTG 3215
             |||   ||| |||||||| ||| |         |      || ||||||||||| |
Db   3095 -AGCCTCGGAGGACCTCTGCCCAGGGA--------GGTGCCATATCTGGCAGGCAGGCCA 3145

Qy   3216 CTCTCTCTCAGGATCACCACGCATCTCAGGATTGGTCTAAACTTCAAGTCTCAACCAAGT 3275
          |||||      ||     | | |||    ||| || | ||||| ||||  | | | | |||
Db   3146 GTCTCT---TAGAATCACCCACATTGTAGGGTTAGCCTAAATTTCAGATTTAACCAAAGC 3202

Qy   3276 GTCTGAAGTGAACTTTGCATTGAATAAATTTTTGCCATGGAAAGAACATCAAACAAGCCA 3335
            ||  |                |||| |||||| || || |  | ||     | |||||
Db   3203 CACTTCA--------------CCTTAAACTTTTGCAATTGAGAAGAAATTGGTC-AGCCA 3247

Qy   3336 CTCATCTCTACAGAGATAAGAAAACAAGTTTGGCAGAGCAAGAGACAGAAGACCGTGGAG 3395
            |  |||| |||  | |  || ||| ||    | ||||  ||  |||||||||  | |
Db   3248 AGCCCCTCTGCAGGAACACCAAGACAGGTCCAGTAGAGTTAGGAACAGAAGACGGAG--- 3304

Qy   3396 AAATCAGAAGGGGGAACAGTCAGTTTAGTTAAGGATGGAACCTGGGAAAGGCCACCATTC 3455
                              | |    |  || | |  |||||||| ||||||||||  |
Db   3305 ------------------TTAACAAGAAGTGAGAAGGAAACCTGGGAGAGGCCACCATCC 3346

Qy   3456 CTGCTTGATGGGGCTCTGATTTGCTCTTGCTCAAGTGGAATAAAACCCCATGGTCTTCTT 3515
            ||| | |||| || | || |||||||| |||| |||  ||     |    | |
Db   3347 A---GTGAGGCGGCTGTGCTCTGTTCTTGCTCAGGTGGTATAAGACCTGGAGTCTTCCAG 3403

Qy   3516 GACATGATTCTTGATCTTTTCTCCACTGAGACACACTTAAGTGATGATCCTTACAGGACT 3575
          | ||||   || || |||||||||||||| | ||||   |  ||||||||||  ||| ||
Db   3404 GGCATG--CCTGGACCTTTTCTCCACTGACATACAC---ACAGATGATCCTTCTAGGTCT 3458

Qy   3576 GACACCCTAATGCCAATAAAAGTTGCTCATTATGGACTGC 3615
            |     ||||||||| ||| |||||||| ||||| ||||
Db   3459 TA-----TAATGCCAACAAAGGTTGCTCACTATGGGCTGC 3493
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RESULT 7
AAC90030
ID   AAC90030 standard; cDNA; 1782 BP.
XX
AC   AAC90030;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Clone HOHEC84 coding sequence #2.
XX
KW   Gene therapy; human; bone morphogenic protein; cancer;
KW   chromosome identification; neural disorder; immune; muscular;
KW   reproductive; gastrointestinal; pulmonary; cardiovascular; renal;
KW   proliferative; wound healing; infectious disease; thrombosis; arthritis;
KW   infertility; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061774-A2.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US09028.
XX
PR   09-APR-1999;   99US-0128701.
PR   23-APR-1999;   99US-0130693.
PR   29-APR-1999;   99US-0131672.
PR   11-JUN-1999;   99US-0138632.
PR   03-AUG-1999;   99US-0147020.
PR   09-SEP-1999;   99US-0152933.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Komatsoulis G,  Rosen CA,  Shi Y;
XX
DR   WPI; 2000-656328/63.
DR   P-PSDB; AAB49538.
XX
PT   Bone morphogenic proteins and nucleic acid sequences encoding them,
PT   useful for detecting, preventing and treating cancers and neurological,
PT   immune system and cardiovascular disorders -
XX
PS   Claim 1; Pages 274-275; 291pp; English.
XX
CC   The present invention relates to isolated coding sequences and proteins
CC   for human bone morphogenic proteins (BMPs) (see AAC90025-C90030 and
CC   AAB49533-B49538). The present sequence is one such coding sequence. This
CC   sequence may be used for detection of various disorders such as cancer,
CC   for chromosome identification, as chromosome markers and for numerous
CC   other diagnostic or research purposes. In addition, this sequence may be
CC   used to treat disorders such as neural, immune, muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders (numerous examples of each type of disorder are given in the
CC   specification), wounds, infectious diseases, thrombosis, arthritis, and
CC   infertility.
XX
SQ   Sequence 1782 BP; 326 A; 524 C; 616 G; 316 T; 0 other;

  Query Match             47.5%;  Score 1718.2;  DB 21;  Length 1782;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1754;  Conservative    0;  Mismatches   23;  Indels    2;  Gaps    2;

Qy      60 CAAGCCCCCTCTTTCCTAGCCTGGACAGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 119
             ||  |||   || |||  ||      | ||||||||||||||||||||||||||||||||
Db       3 CAGCCCCGGACTGTCCGCGCTCCATCTGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 62

Qy     120 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 122

Qy     180 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 182
```

```
Qy    240 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 299
Db    183 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 242

Qy    300 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 359
Db    243 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 302

Qy    360 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 419
Db    303 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 362

Qy    420 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 479
Db    363 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 422

Qy    480 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 539
Db    423 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 482

Qy    540 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGG 599
Db    483 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCA-GGCCGGCGGCTGGAGGAGGT-CGG 540

Qy    600 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 659
Db    541 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 600

Qy    660 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGC 719
Db    601 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGC 660

Qy    720 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 779
Db    661 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 720

Qy    780 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAAT 839
Db    721 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAAT 780

Qy    840 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 899
Db    781 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 840

Qy    900 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 959
Db    841 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 900

Qy    960 CATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAA 1019
Db    901 CACGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAA 960

Qy   1020 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGC 1079
Db    961 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGC 1020

Qy   1080 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1139
Db   1021 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1080

Qy   1140 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1199
Db   1081 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1140

Qy   1200 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGC 1259
Db   1141 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGC 1200

Qy   1260 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1319
Db   1201 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1260

Qy   1320 CAACATGAGAATGCTGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGAATCAG 1379
Db   1261 CAACATGAGAATGATGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGAATCAG 1320

Qy   1380 GTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCTATTGGAGGTGCAGGTGGAGGTG 1439
Db   1321 GTGCGCTTGGCTGGTGGGCGTATCCCTGAAGAGGGGCTATTGGAGGTGCAGGTGGAGGTG 1380

Qy   1440 AACGGGGTCCCACGCTGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1499
Db   1381 AACGGGGTCCCACGCTGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1440

Qy   1500 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATCCCTACAAGGAAACCTGGTTC 1559
Db   1441 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCTGGTTC 1500

Qy   1560 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1619
Db   1501 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1560

Qy   1620 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1679
Db   1561 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1620

Qy   1680 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1739
Db   1621 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1680

Qy   1740 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1799
Db   1681 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1740

Qy   1800 GAGGAGAACTGCCTCTCCAAGTCTGCGGATCACATGGAC 1838
Db   1741 GAGGAGAACTGCCTCTCCAAGTCTGCGGTCGACGCGGCC 1779
```

RESULT 8
AAC93436
ID   AAC93436 standard; cDNA; 1782 BP.
XX
AC   AAC93436;
XX
DT   16-FEB-2001 (first entry)
XX
DE   Human secreted protein gene 15 SEQ ID NO:25.
XX
KW   Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW   antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW   nootropic; neuroprotective; antibacterial; virucide; fungicide;
KW   opthalmalogical; vulnerary; autoimmune disease; rheumatoid arthritis;
KW   hyperproliferative disorders; cancer; cardiovascular disorder;
KW   cardiac arrest; cerebrovascular disorder; nervous system disorder;
KW   Alzheimer's disease; ocular disorder; wound healing; skin aging; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061625-A1.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US08981.
XX
PR   09-APR-1999;   99US-0128701.
PR   20-JAN-2000; 2000US-0177166.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Rosen CA, Ruben SM, Komatsoulis G;
XX
DR   WPI; 2000-619226/59.
DR   P-PSDB; AAB51741.

XX
PT New nucleic acid molecules encoding 48 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Claim 1; Page 420; 500pp; English.
XX
CC Polynucleotide sequences AAC93422 - AAC93449 represent cDNA encoding
CC human secreted proteins AAB51724 - AAB51777. Sequences AAB51778 -
CC AAB51825 represent alternative polypeptides encoded by the genes, and
CC amino acid sequences to which they are homologous. The genes and proteins
CC have activities dependent on the tissues and cells in which they are
CC expressed. Examples of their activities include immunosuppressive;
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
CC virucide; fungicide; opthalmalogical; and vulnerary. The secreted
CC proteins, polynucleotides, antagonists and agonists may be useful in
CC treating, preventing and/or diagnosing diseases and disorders such as
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. Oligonucleotide AAC93413 - AAC93421 and peptide AAB51723 are
CC used in the isolation and characterisation of the proteins and
CC polynucleotides of the invention.
XX
SQ Sequence 1782 BP; 326 A; 524 C; 616 G; 316 T; 0 other;

Query Match 47.5%; Score 1718.2; DB 21; Length 1782;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1754; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

```
Qy      60 CAAGCCCCCTCTTTCCTAGCCTGGACAGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 119
           ||  |||   ||  |||  ||     | ||||||||||||||||||||||||||||||||
Db       3 CAGCCCCGGACTGTCCGCGCTCCATCTGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 62

Qy     120 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 122

Qy     180 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 182

Qy     240 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 242

Qy     300 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 302

Qy     360 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     303 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 362

Qy     420 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 422

Qy     480 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 482

Qy     540 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGG 599
           |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||
Db     483 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCA-GGCCGGCGGCTGGAGGAGGT-CGG 540

Qy     600 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 600

Qy     660 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGC 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGC 660

Qy     720 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 720

Qy     780 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAAT 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAAT 780

Qy     840 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 840

Qy     900 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 900

Qy     960 CATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAA 1019
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CACGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAA 960

Qy    1020 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGC 1079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGC 1020

Qy    1080 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1080

Qy    1140 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1140

Qy    1200 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGC 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGC 1200

Qy    1260 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1260

Qy    1320 CAACATGAGAATGCTGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGAATCAG 1379
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 CAACATGAGAATGATGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGAATCAG 1320

Qy    1380 GTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCTATTGGAGGTGCAGGTGGAGGTG 1439
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     1321 GTGCGCTTGGCTGGTGGGCGTATCCCTGAAGAGGGGCTATTGGAGGTGCAGGTGGAGGTG 1380

Qy    1440 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1440

Qy    1500 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCTGGTTC 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCTGGTTC 1500

Qy    1560 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1560

Qy    1620 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1679
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1561 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1620

Qy   1680 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1680

Qy   1740 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1740

Qy   1800 GAGGAGAACTGCCTCTCCAAGTCTGCGGATCACATGGAC 1838
          ||||||||||||||||||||||||||||  ||  || |
Db   1741 GAGGAGAACTGCCTCTCCAAGTCTGCGGTCGACGCGGCC 1779
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RESULT 9
AAC90026
ID   AAC90026 standard; cDNA; 1781 BP.
XX
AC   AAC90026;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Clone HOHEC84 coding sequence #1.
XX
KW   Gene therapy; human; bone morphogenic protein; cancer;
KW   chromosome identification; neural disorder; immune; muscular;
KW   reproductive; gastrointestinal; pulmonary; cardiovascular; renal;
KW   proliferative; wound healing; infectious disease; thrombosis; arthritis;
KW   infertility; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061774-A2.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US09028.
XX
PR   09-APR-1999;   99US-0128701.
PR   23-APR-1999;   99US-0130693.
PR   29-APR-1999;   99US-0131672.
PR   11-JUN-1999;   99US-0138632.
PR   03-AUG-1999;   99US-0147020.
PR   09-SEP-1999;   99US-0152933.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Komatsoulis G,  Rosen CA,  Shi Y;
XX
DR   WPI; 2000-656328/63.
DR   P-PSDB; AAB49534.
XX
PT   Bone morphogenic proteins and nucleic acid sequences encoding them,
PT   useful for detecting, preventing and treating cancers and neurological,
PT   immune system and cardiovascular disorders -
XX
PS   Claim 1; Page 271; 291pp; English.
XX
CC   The present invention relates to isolated coding sequences and proteins
CC   for human bone morphogenic proteins (BMPs) (see AAC90025-C90030 and
CC   AAB49533-B49538). The present sequence is one such coding sequence. This
CC   sequence may be used for detection of various disorders such as cancer,
CC   for chromosome identification, as chromosome markers and for numerous
CC   other diagnostic or research purposes. In addition, this sequence may be
CC   used to treat disorders such as neural, immune, muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders (numerous examples of each type of disorder are given in the
CC   specification), wounds, infectious diseases, thrombosis, arthritis, and
CC   infertility.
XX
SQ   Sequence 1781 BP; 326 A; 524 C; 615 G; 316 T; 0 other;
```

```
Query Match             47.3%;  Score 1711.4;  DB 21;  Length 1781;
Best Local Similarity   98.4%;  Pred. No. 0;
Matches 1750;  Conservative    0;  Mismatches   26;  Indels    3;  Gaps    2;

Qy      60 CAAGCCCCCTCTTTCCTAGCCTGGACAGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC 119
           ||  |||   ||  |||  ||      | ||||||||||||||||||||||||||||||||
Db       3 CAGCCCCGGACTGTCCGCGCTCCATCTGGTATCTTGGCCTCAGCTGTCCTTGAAGTCACC  62

Qy     120 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 179
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ATGGCGTGGTCCCCACCAGCCACCCTCTTTCTGTTCCTGCTGCTGCTAGGCCAGCCCCCT 122

Qy     180 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 CCCAGCAGGCCACAGTCACTGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAG 182

Qy     240 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 299
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     183 CCAGAGGAGGGCCGCCTGGAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGAC 242

Qy     300 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 359
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     243 AACTTTGCTATCCAGGAGGCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTG 302

Qy     360 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 419
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     303 ACCTGGGCCCACAGTGCCAAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTG 362

Qy     420 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 CGCTGTGTGGGCACAGAGAGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGT 422

Qy     480 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 539
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 GACTGCAGTCACTCAGAAGACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTAC 482

Qy     540 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGG 599
           |||||||||||||||||||||||||||||||||||||| |||||||||||||  |  |||
Db     483 CTTTCTGAAACTGTCTCCAATGCCCTTGGGCCCCA-GGCCGGCGGCTGGAG--AGGTCGG 539

Qy     600 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 659
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 CTCAAGCCCATCCTTGCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAG 599

Qy     660 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCACGGCTGGACCATGAACAACAGC 719
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GTGAAGTATGAGGGCCACTGGCGGCAGGTGTGTGACCACGGCTGGACCATGAACAACAGC 659

Qy     720 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 779
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     660 AGGGTGGTGTGCGGGATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTAC 719

Qy     780 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAAT 839
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     720 AGGAAAGTCTGGGATCTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAAT 779

Qy     840 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 899
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     780 AAGAACTCCTTCTGGATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAAC 839

Qy     900 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 959
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     840 TGCCAGGTGCAGGTGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATG 899

Qy     960 CATGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAA 1019
           || ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     900 CACGCTGTGGTCAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAA 959

Qy    1020 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTCGCTCCGGGGCCCAGGTGGGC 1079
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     960 CGCAAAGGGTCCTGGGCAGAGGAGCCGAGGGTGCGCCTCGCTCCGGGGCCCAGGTGGGC 1019

Qy    1080 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGCCACGGTCTGTGACCACAGGTGG 1139
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```
Db   1020 GAGGGCCGGGTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGG 1079

Qy   1140 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 AACCTCATCTCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCC 1139

Qy   1200 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 CTCTTTGGGGCCCGGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGC 1199

Qy   1260 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGGGATATGAGCGGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGC 1259

Qy   1320 CAACATGAGAATGCTGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGAATCAG 1379
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 CAACATGAGAATGATGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGAATCAG 1319

Qy   1380 GTGCGCTTGGCTGGTGGGCGTATCCCTGAGGAGGGGCTATTGGAGGTGCAGGTGGAGGTG 1439
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1320 GTGCGCTTGGCTGGTGGGCGTATCCCTGAAGAGGGGCTATTGGAGGTGCAGGTGGAGGTG 1379

Qy   1440 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 AACGGGGTCCCACGCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATG 1439

Qy   1500 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCTGGTTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 GTGGCCTGCCGACAGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCTGGTTC 1499

Qy   1560 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 TGGTCGGGGACGCCAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACA 1559

Qy   1620 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 GAGCTGGCCCTGCAGCAGTGCCAGAGGCACGGGCCGGTGCACTGCTCCCACGGTGGCGGG 1619

Qy   1680 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 CGCTTCCTGGCTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAG 1679

Qy   1740 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CTAGTGCAGGAGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCAC 1739

Qy   1800 GAGGAGAACTGCCTCTCCAAGTCTGCGGATCACATGGAC 1838
          |||||||||||||||||||||||||    ||  || |
Db   1740 GAGGAGAACTGCCTCTCCAAGTCTGCGGTCGACGCGGCC 1778
```

RESULT 10
ABV23110
ID ABV23110 standard; cDNA; 3748 BP.
XX
AC ABV23110;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 23101.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 4134-4135; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ Sequence 3748 BP; 868 A; 1089 C; 1085 G; 695 T; 11 other;

Query Match 23.6%; Score 853.8; DB 23; Length 3748;
Best Local Similarity 63.8%; Pred. No. 1.2e-211;
Matches 1400; Conservative 0; Mismatches 742; Indels 51; Gaps 5;

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Qy    199 TGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAGCCAGAGGAGGGCCGCCTGG 258
          ||| ||  | | |||| || ||||  || |   |||| |||      ||||||||  |||
Db    452 TGGCCAAGATTCAGCTGCGCCTGGCTGGGCAGAAGAGGAAGCACAGCGAGGGCCGGGTGG 511

Qy    259 AGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGACAACTTTGCTATCCAGGAGG 318
          |||||    |  | ||||||||||||||||||| |||||| ||||  | |||||  |  |
Db    512 AGGTGTACTATGATGGCCAGTGGGGCACCGTGTGCGATGACGACTTCTCCATCCACGCTG 571

Qy    319 CCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTGACCTGGGCCCACAGTGCCA 378
          ||   || |  |||||  |||||||| ||  |  |||  | |||||  |   |||  ||
Db    572 CCCACGTCGTCTGCCGGGAGCTGGGCTACGTGGAGGCCAAGTCCTGGACTGCCAGCTCCT 631

Qy    379 AGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTGCGCTGTGTGGGCACAGAGA 438
            |||||| | || || || |||||||| | ||||||  | |  ||||   ||||  |||
Db    632 CCTACGGCAAGGGAGAAGGGCCCATCTGGTTAGACAATCTCCACTGTACTGGCAACGAGG 691

Qy    439 GCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGTGACTGCAGTCACTCAGAAG 498
            || | |      |||   || |||||||||||| |||| ||||||||  ||| | || |
Db    692 CGACCCTTGCAGCATGCACCTCCAATGGCTGGGGCGTCACTGACTGCAAGCACACGGAGG 751

Qy    499 ACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTACCTTTCTGAAACTG---TCT 555
          | || || ||| | |||  |  |     |  || ||| | |   | ||| | |     |
Db    752 ATGTCGGTGTGGTGTGCAGCGACAAAAGGATTCCTGGGTTCAAATTTGACAATTCGTTGA 811

Qy    556 CCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGGCTCAAGCCCATCCTTG 615
           |||      | | |  || |       | | |||||||  | ||| |      |||||||
Db    812 TCAACCAGATAGAGAACCTGAATATCCAGGTGGAGGACATTCGGATTCGAGCCATCCTCT 871

Qy    616 CCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAGGTGAAGTATGAGGGCC 675
          | |     |   ||| | ||||||||  |||||   ||||||||||||| | |
Db    872 CAACCTACCGCAAGCGCACCCCAGTGATGGAGGGCTACGTGGAGGTGAAGGAGGGCAAGA 931
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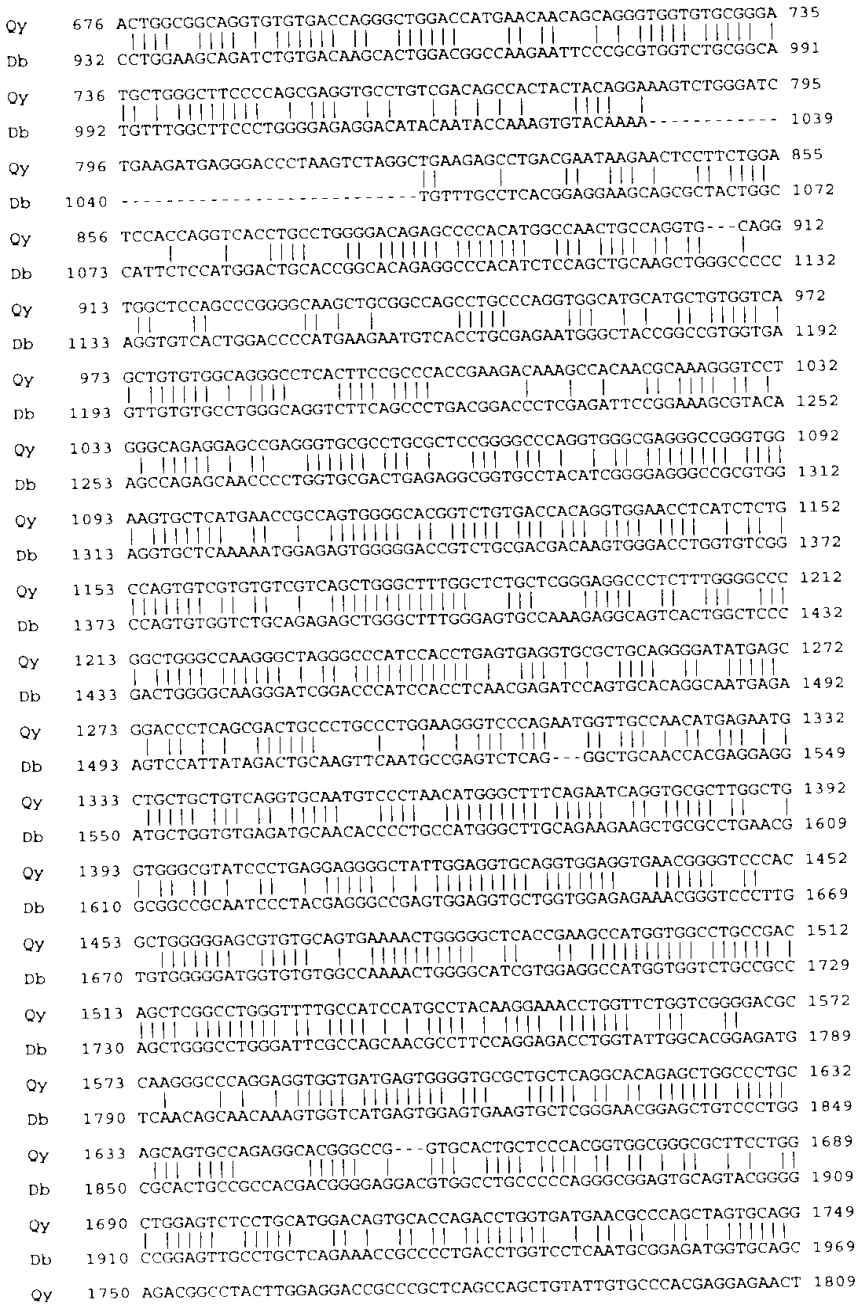

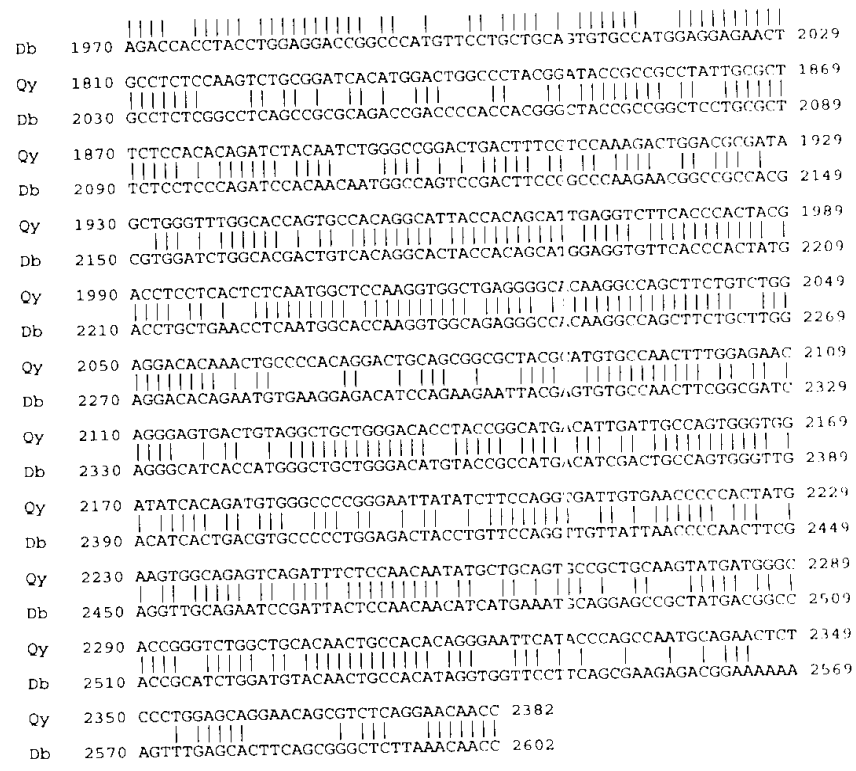

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RESULT 11
ABV28948
ID   ABV28948 standard; cDNA; 3748 BP.
XX
AC   ABV28948;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 28939
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
```
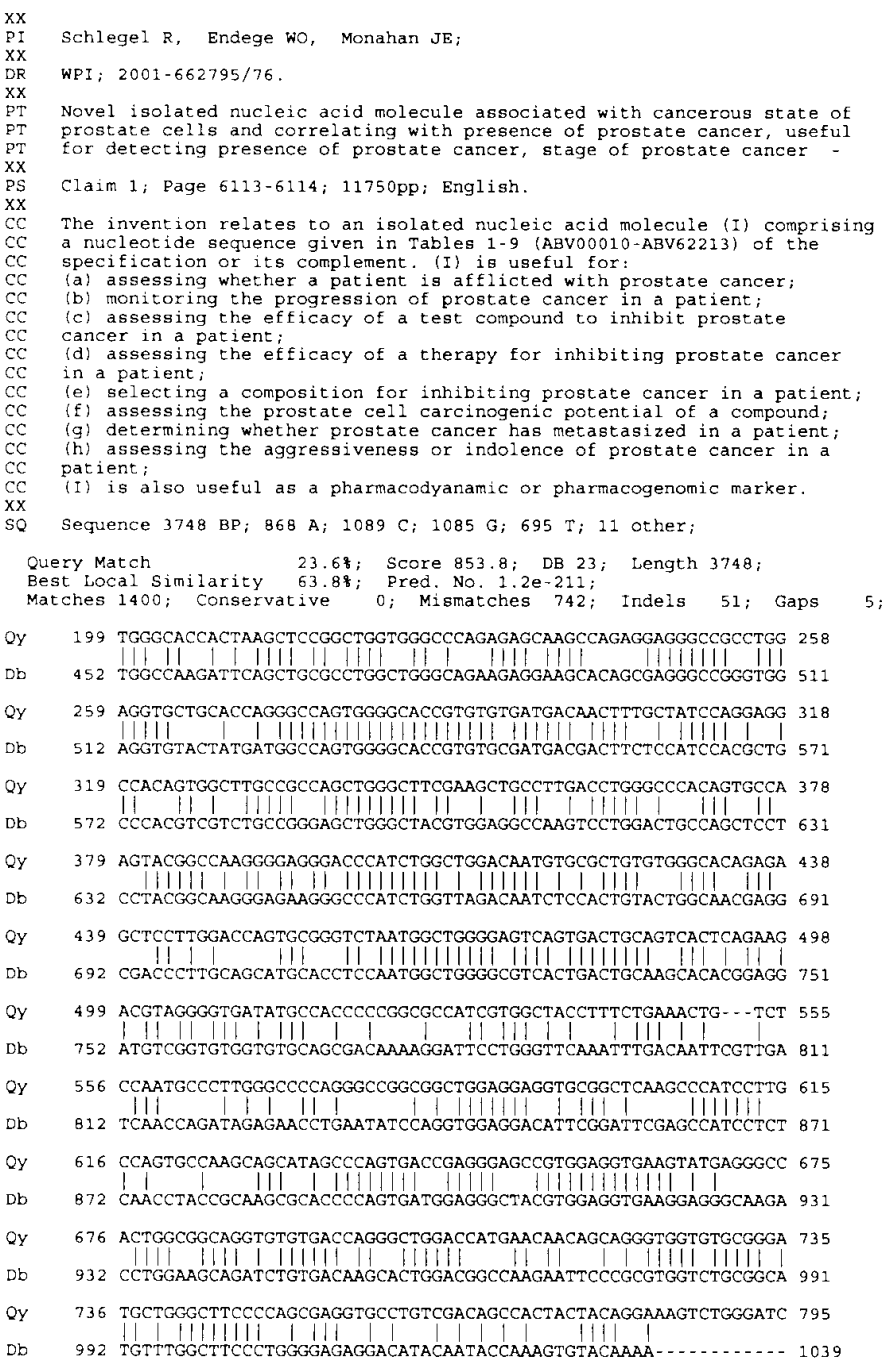
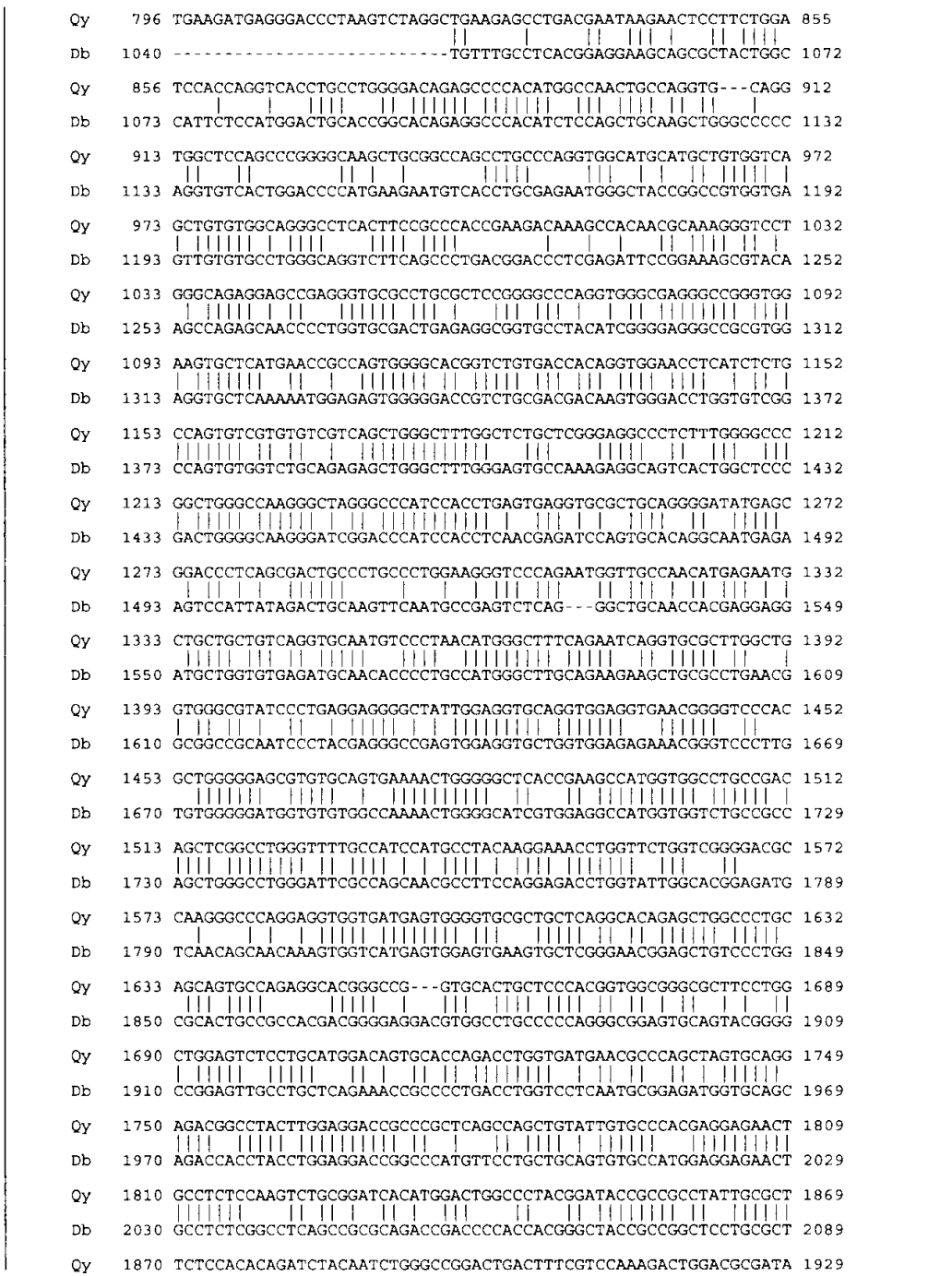

XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 6113-6114; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ Sequence 3748 BP; 868 A; 1089 C; 1085 G; 695 T; 11 other;

Query Match 23.6%; Score 853.8; DB 23; Length 3748;
Best Local Similarity 63.8%; Pred. No. 1.2e-211;
Matches 1400; Conservative 0; Mismatches 742; Indels 51; Gaps 5;





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Db    2090 TCTCCTCCCAGATCCACAACAATGGCCAGTCCGACTTCCGGCCCAAGAACGGCCGCCACG 2149

Qy    1930 GCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGGTCTTCACCCACTACG 1989

Db    2150 CGTGGATCTGGCACGACTGTCACAGGCACTACCACAGCATGGAGGTGTTCACCCACTATG 2209

Qy    1990 ACCTCCTCACTCTCAATGGCTCCAAGGTGGCTGAGGGGCACAAGGCCAGCTTCTGTCTGG 2049

Db    2210 ACCTGCTGAACCTCAATGGCACCAAGGTGGCAGAGGGCCACAAGGCCAGCTTCTGCTTGG 2269

Qy    2050 AGGACACAAACTGCCCCACAGGACTGCAGCGGCGCTACGCATGTGCCAACTTTGGAGAAC 2109

Db    2270 AGGACACAGAATGTGAAGGAGACATCCAGAAGAATTACGAGTGTGCCAACTTCGGCGATC 2329

Qy    2110 AGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACATTGATTGCCAGTGGGTGG 2169

Db    2330 AGGGCATCACCATGGGCTGCTGGGACATGTACCGCCATGACATCGACTGCCAGTGGGTTG 2389

Qy    2170 ATATCACAGATGTGGGCCCCGGGAATTATATCTTCCAGGTGATTGTGAACCCCCACTATG 2229

Db    2390 ACATCACTGACGTGCCCCCTGGAGACTACCTGTTCCAGGTTGTTATTAACCCCAACTTCG 2449

Qy    2230 AAGTGGCAGAGTCAGATTTCTCCAACAATATGCTGCAGTGCCGCTGCAAGTATGATGGGC 2289

Db    2450 AGGTTGCAGAATCCGATTACTCCAACAACATCATGAAATGCAGGAGCCGCTATGACGGCC 2509

Qy    2290 ACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATACCCAGCCAATGCAGAACTCT 2349

Db    2510 ACCGCATCTGGATGTACAACTGCCACATAGGTGGTTCCTTCAGCGAAGAGACGGAAAAAA 2569

Qy    2350 CCCTGGAGCAGGAACAGCGTCTCAGGAACAACC 2382

Db    2570 AGTTTGAGCACTTCAGCGGGCTCTTAAACAACC 2602
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RESULT 12
ABQ88183
ID ABQ88183 standard; cDNA; 3432 BP.
XX
AC ABQ88183;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human osteoblast differentiation related cDNA SEQ ID NO 90.
XX
KW Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW osteoporosis; osteopathic; ss.
XX
OS Homo sapiens.
XX
PN WO200250301-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-US48276.
XX
PR 18-DEC-2000; 2000US-255882P.
PR 24-APR-2001; 2001US-285691P.
XX
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
PI Mertz L;
XX
DR WPI; 2002-557663/59.
XX
PT Use of genes and their expression profiles associated with osteoblast
PT differentiation for screening modulators bone formation, for diagnosing
PT or treating e.g. osteoporosis, or as markers for the differentiation
PT process -
XX

PS Claim 1; SEQ ID NO 90; 78pp + Sequence Listing; English.
XX
CC The invention relates to genes and their expression profiles are used
CC for:
CC (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition;
CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC osteoblast formation or osteoporosis; or
CC (c) treating or monitoring treatment of the conditions cited in (b), or
CC monitoring the progression of bone tissue deposition.
CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
CC drug-induced abnormalities in bone formation or bone loss, conditions
CC that involve altered bone metabolism (e.g. idiopathic juvenile
CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC osteoblast differentiation associated cDNA marker of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3432 BP; 775 A; 1007 C; 983 G; 667 T; 0 other;

Query Match 23.5%; Score 849; DB 24; Length 3432;
Best Local Similarity 63.7%; Pred. No. 2.1e-210;
Matches 1397; Conservative 0; Mismatches 745; Indels 51; Gaps 5;

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Qy     199 TGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAGCCAGAGGAGGGCCGCCTGG 258

Db     405 TGGCCAAGATTCAGCTGCGCCTGGCTGGGCAGAAGAGGAAGCACAGCGAGGGCCGGGTGG 464

Qy     259 AGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGACAACTTTGCTATCCAGGAGG 318

Db     465 AGGTGTACTATGATGGCCAGTGGGGCACCGTGTGCGATGACGACTTCTCCATCCACGCTG 524

Qy     319 CCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTGACCTGGGCCCACAGTGCCA 378

Db     525 CCCACGTCGTCTGCCGGGAGCTGGGCTATGTGGAGGCCAAGTCCTGGACTGCCAGCTCCT 584

Qy     379 AGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTGCGCTGTGTGGGCACAGAGA 438

Db     585 CCTACGGCAAGGGAGAAGGGCCCATCTGGTTAGACAATCTCCACTGTACTGGCAACGAGG 644

Qy     439 GCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGTGACTGCAGTCACTCAGAAG 498

Db     645 CGACCCTTGCAGCATGCACCTCCAATGGCTGGGGCGTCACTGACTGCAAGCACACGGAGG 704

Qy     499 ACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTACCTTTCTGAAACTG---TCT 555

Db     705 ATGTCGGTGTGGTGTGCAGCGACAAAAGGATTCCTGGGTTCAAATTTGACAATTCGTTGA 764

Qy     556 CCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGCTGCGGCTCAAGCCCATCCTTG 615

Db     765 TCAACCAGATAGAGAACCTGAATATCCAGGTGGAGGACATTCGGATTCGAGCCATCCTCT 824

Qy     616 CCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCCTGGAGGTGAAGTATGAGGGCC 675

Db     825 CAACCTACCGCAAGCGCACCCCAGTGATGGAGGGCTACCTGGAGGTGAAGGAGGGCAAGA 884

Qy     676 ACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGCAGGGTGGTGTGCGGGA 735

Db     885 CCTGGAAGCAGATCTGTGACAAGCACTGGACGGCCAAGAATTCCCGCGTGGTCTGCGGCA 944

Qy     736 TGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTACAGGAAAGTCTGGGATC 795

Db     945 TGTTTGGCTTCCCTGGGGAGAGGACATACAATACCAAAGTGTACAAAA---- ------- 992

Qy     796 TGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAATAAGAACTCCTTCTGGA 855

Db     993 ----------------------------TGTTTGCCTCACGGAGGAAGCAGCGCTACTGGC 1025

Qy     856 TCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAACTGCCAGGTG---CAGG 912
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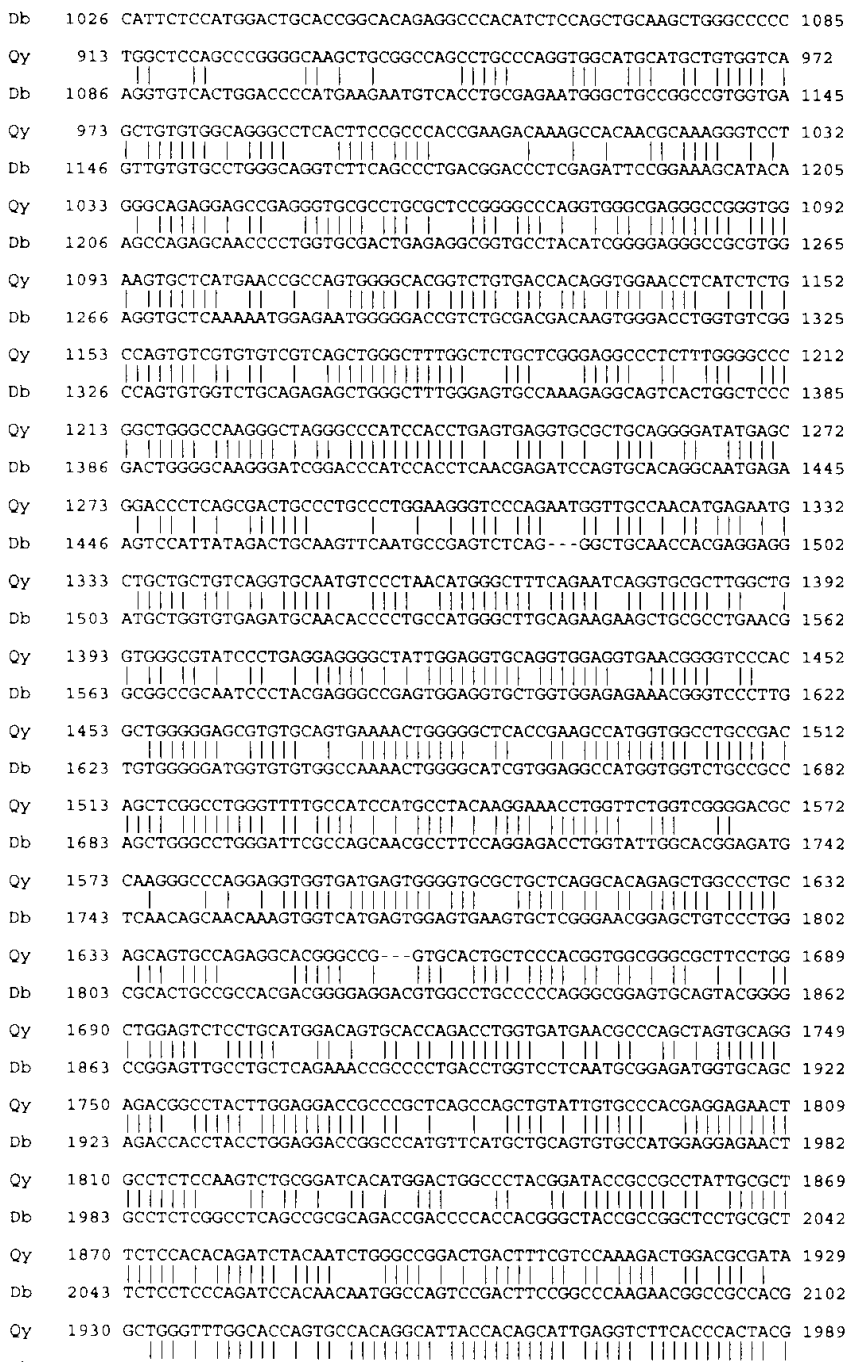

RESULT 13
ABA95142
ID ABA95142 standard; cDNA; 2325 BP.
XX
AC ABA95142;
XX
DT 20-MAY-2002 (first entry)
XX
DE Human LOR-1 protein encoding cDNA.
XX
KW Lysyl-oxidase; angiogenesis; cancer; LOR-1; antiarthritic; antidiabetic;
KW ophthalmological; antipsoriatic; antiinflammatory; vasotropic; human;
KW immunomodulator; dermatological; vulnerary; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2325
FT /*tag= a
FT /product= "LOR-1 protein"
XX
PN WO200211667-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-IL00728.
XX
PR 08-AUG-2000; 2000US-223739P.
XX
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
PI Neufeld G, Akiri G, Vadasz Z, Gengrovitch S;
XX
DR WPI; 2002-227109/28.
DR P-PSDB; ABB07649.
XX
PT Composition for modulating angiogenesis in mammalian tissue for
PT treating e.g. arthritis, psoriasis, comprises molecule capable of
PT modifying level and/or activity of at least one type of lysyl-oxidase
PT of the tissue -
XX
PS Claim 5; Page 49-50; 67pp; English.
XX

CC The invention provides a pharmaceutical composition useful for modulating
CC angiogenesis in mammalian tissue. The composition comprises a molecule
CC capable of modifying a level and/or activity of at least one type of
CC lysyl-oxidase of the mammalian tissue as an active ingredient and a
CC carrier. Methods for identifying molecules capable of modulating
CC angiogenesis; for modulating angiogenesis in a mammalian tissue; and for
CC determining the malignancy of cancerous tissue are also provided, where
CC the modulation in activity is useful for treating arthritis, diabetic
CC retinopathy, psoriasis, vasculitis; and for disease characterized by
CC fragile blood vessels, including Marfans syndrome, Kawasaki, Ehlers-
CC Danlos, cutis-laxa, and takysu; diseases characterized by changes in the
CC wall of blood vessels e.g. restenosis which is a common complication
CC following balloon therapy, fibromuscular dysplasia and aortic stenosis.
CC The present sequence represents a cDNA encoding a LOR-1 protein,
CC belonging to the lysyl-oxidase family of enzymes.
XX
SQ Sequence 2325 BP; 522 A; 670 C; 717 G; 416 T; 0 other;

Query Match 23.4%; Score 847.4; DB 24; Length 2325;
Best Local Similarity 63.7%; Pred. No. 4.5e-210;
Matches 1396; Conservative 0; Mismatches 746; Indels 51; Gaps 5;

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Qy   199 TGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAGCCAGAGGAGGGGCCGCCTGG 258
Db   158 TGGCCAAGATTCAGCTGCGCCTGGCTGGGCAGAAGAGGAAGCACAGCGAGGGCCGGGTGG 217

Qy   259 AGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGACAACTTTGCTATCCAGGAGG 318
Db   218 AGGTGTACTATGATGGCCAGTGGGGCACCGTGTGCGATGACGACTTCTCCATCCACGCTG 277

Qy   319 CCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTGACCTGGGCCCACAGTGCCA 378
Db   278 CCCACGTCGTCTGCCGGGAGCTGGGCTATGTGGAGGCCAAGTCCTGGACTGCCAGCTCCT 337

Qy   379 AGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTGCGCTGTGTGGGCACAGAGA 438
Db   338 CCTACGGCAAGGGAGAAGGGCCCATCTGGTTAGACAATCTCCACTGTACTGGCAACGAGG 397

Qy   439 GCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGTGACTGCAGTCACTCAGAAG 498
Db   398 CGACCCTTGCAGCATGCACCTCCAATGGCTGGGGCGTCACTGACTGCAAGCACACGGAGG 457

Qy   499 ACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTACCTTTCTGAAACTG---TCT 555
Db   458 ATGTCGGTGTGGTGTGCAGCGACAAAAGGATTCCTGGGTTCAAATTTGACAATTCGTTGA 517

Qy   556 CCAATGCCCTTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGGCTCAAGCCCATCCTTG 615
Db   518 TCAACCAGATAGAGAACCTGAATATCCAGGTGGAGGACATTCGGATTCGAGCCATCCTCT 577

Qy   616 CCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGGAGCCGTGGAGGTGAAGTATGAGGGCC 675
Db   578 CAACCTACCGCAAGCGCACCCCCGTGATGGAGGGCTACGTGGAGGTGAAGGAGGGCAAGA 637

Qy   676 ACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGCAGGGTGGTGTGCGGGA 735
Db   638 CCTGGAAGCAGATCTGTGACAAGCACTGGACGGCCAAGAATTCCCGCGTGGTCTGCGGCA 697

Qy   736 TGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTACAGGAAAGTCTGGGATC 795
Db   698 TGTTTGGCTTCCCTGGGGAGAGGACATACAATACCAAAGTGTACAAAA---------- 745

Qy   796 TGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAATAAGAACTCCTTCTGGA 855
Db   746 ----------TGTTTGCCTCACGGAGGAAGCAGCGCTACTGGC 778

Qy   856 TCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAACTGCCAGGTG---CAGG 912
Db   779 CATTCTCCATGGACTGCACCGGCACAGAGGCCCACATCTCCAGCTGCAAGCTGGGCCCCC 838

Qy   913 TGGCTCCAGCCCGGGGCAAGCTGCGGCCAGCCTGCCCAGGTGGCATGCATGCTGTGGTCA 972
Db   839 AGGTGTCACTGGACCCCATGAAGAATGTCACCTGCGAGAATGGGCTGCCGGCCGTGGTGA 898

Qy   973 GCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAACGCAAAGGGTCCT 1032
Db   899 GTTGTGTGCCTGGGCAGGTCTTCAGCCCTGACGGACCCTCGAGATTCCGGAAAGCATACA 958

Qy  1033 GGGCAGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGCGAGGGCCGGGTGG 1092
Db   959 AGCCAGAGCAACCCCTGGTGCGACTGAGAGGCGGTGCCTACATCGGGGAGGGCCGCGTGG 1018

Qy  1093 AAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGGAACCTCATCTCTG 1152
Db  1019 AGGTGCTCAAAAATGGAGAATGGGGGACCGTCTGCGACGACAAGTGGGACCTGGTGTCGG 1078

Qy  1153 CCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCCGGGAGGCCCTCTTTGGGGCCC 1212
Db  1079 CCAGTGTGGTCTGCAGAGAGCTGGGCTTTGGGAGTGCCAAAGAGGCAGTCACTGGCTCCC 1138

Qy  1213 GGCTGGGCCAAGGGCTAGGGCCCATCCACCTGAGTGAGGTGCGCTGCAGGGGATATGAGC 1272
Db  1139 GACTGGGGCAAGGGATCGGACCCATCCACCTCAACGAGATCCAGTGCACAGGCAATGAGA 1198

Qy  1273 GGACCCTCAGCGACTGCCCTGCCCTGGAAGGGTCCCAGAATGGTTGCCAACATGAGAATG 1332
Db  1199 AGTCCATTATAGACTGCAAGTTCAATGCCGAGTCTCAG---GGCTGCAACCACGAGGAGG 1255

Qy  1333 CTGCTGCTGTCAGGTGCAATGTCCCTAACATGGGCTTTCAGAATCAGGTGCGCTTGGCTG 1392
Db  1256 ATGCTGGTGTGAGATGCAACACCCCTGCCATGGGCTTGCAGAAGAAGCTGCGCCTGAACG 1315

Qy  1393 GTGGGCGTATCCCTGAGGAGGGGCTATTGGAGGTGCAGGTGGAGGTGAACGGGGTCCCAC 1452
Db  1316 GCGGCCGCAATCCCTACGAGGGCCGAGTGGAGGTGCTGGTGGAGAGAAACGGGTCCCTTG 1375

Qy  1453 GCTGGGGGAGCGTGTGCAGTGAAAACTGGGGGCTCACCGAAGCCATGGTGGCCTGCCGAC 1512
Db  1376 TGTGGGGGATGGTGTGTGGCCAAAACTGGGGCATCGTGGAGGCCATGGTGGTCTGCCGCC 1435

Qy  1513 AGCTCGGCCTGGGTTTTGCCATCCATGCCTACAAGGAAACCTGGTTCTGGTCGGGGACGC 1572
Db  1436 AGCTGGGCCTGGGATTCGCCAGCAACGCCTTCCAGGAGACCTGGTATTGGCACGGAGATG 1495

Qy  1573 CAAGGGCCCAGGAGGTGGTGATGAGTGGGGTGCGCTGCTCAGGCACAGAGCTGGCCCTGC 1632
Db  1496 TCAACAGCAACAAAGTGGTCATGAGTGGAGTGAAGTGCTCGGGAACGGAGCTGTCCCTGG 1555

Qy  1633 AGCAGTGCCAGAGGCACGGGCCG---GTGCACTGCTCCCACGGTGGCGGGCGCTTCCTGG 1689
Db  1556 CGCACTGCCGCCACGACGGGGAGGACGTGGCCTGCCCCCAGGGCGGAGTGCAGTACGGGG 1615

Qy  1690 CTGGAGTCTCCTGCATGGACAGTGCACCAGACCTGGTGATGAACGCCCAGCTAGTGCAGG 1749
Db  1616 CCGGAGTTGCCTGCTCAGAAACCGCCCCTGACCTGGTCCTCAATGCGGAGATGGTGCAGC 1675

Qy  1750 AGACGGCCTACTTGGAGGACCGCCCGCTCAGCCAGCTGTATTGTGCCCACGAGGAGAACT 1809
Db  1676 AGACCACCTACCTGGAGGACCGGCCCATGTTCATGCTGCAGTGTGCCATGGAGGAGAACT 1735

Qy  1810 GCCTCTCCAAGTCTGCGGATCACATGGACTGGCCCTACGGATACCGCCGCCTATTGCGCT 1869
Db  1736 GCCTCTCGGCCTCAGCCGCGCAGACCGACCCCACCACGAGGCTACCGCCGGCTCCTGCGCT 1795

Qy  1870 TCTCCACACAGATCTACAATCTGGGCCGGACTGACTTTCGTCCAAAGACTGGACGCGATA 1929
Db  1796 TCTCCTCCCAGATCCACAACAATGGCCAGTCCGACTTCCGGCCCAAGAACGGCCGCCACG 1855

Qy  1930 GCTGGGTTTGGCACCAGTGCCACAGGCATTACCACAGCATTGAGGTCTTCACCCACTACG 1989
Db  1856 CGTGGATCTGGCACGACTGTCACAGGCACTACCACAGCATGGAGGTGTTCACCCACTATG 1915

Qy  1990 ACCTCCTCACTCTCAATGGCTCCAAGGTGGCTGAGGGGCACAAGGCCAGCTTCTGTCTGG 2049
Db  1916 ACCTGCTGAACCTCAATGGCACCAAGGTGGCAGAGGGCCACAAGGCCAGCTTCTGCTTGG 1975
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Qy    2050 AGGACACAAACTGCCCCACAGGACTGCAGCGGCGCTACGCATGTGCCAACTTTGGAGAAC 2109
Db    1976 AGGACACAGAATGTGAAGGAGACATCCAGAAGAATTACGAGTGTGCCAACTTCGGCGATC 2035

Qy    2110 AGGGAGTGACTGTAGGCTGCTGGGACACCTACCGGCATGACATTGATTGCCAGTGGGTGG 2169
Db    2036 AGGGCATCACCATGGGCTGCTGGGACATGTACCGCCATGACATCGACTGCCAGTGGGTTG 2095

Qy    2170 ATATCACAGATGTGGGCCCCGGGAATTATATCTTCCAGGTGATTGTGAACCCCCACTATG 2229
Db    2096 ACATCACTGACGTGCCCCCTGGAGACTACCTGTTCCAGGTTGTTATTAACCCCAACTTCG 2155

Qy    2230 AAGTGGCAGAGTCAGATTTCTCCAACAATATGCTGCAGTGCCGCTGCAAGTATGATGGGC 2289
Db    2156 AGGTTGCAGAATCCGATTACTCCAACAACATCATGAAATGCAGGAGCCGCTATGACGGCC 2215

Qy    2290 ACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATACCCAGCCAATGCAGAACTCT 2349
Db    2216 ACCGCATCTGGATGTACAACTGCCACATAGGTGGTTCCTTCAGCGAAGAGACGGAAAAAA 2275

Qy    2350 CCCTGGAGCAGGAACAGCGTCTCAGGAACAACC 2382
Db    2276 AGTTTGAGCACTTCAGCGGGCTCTTAAACAACC 2308
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RESULT 14
AAH98714
ID AAH98714 standard; cDNA; 3467 BP.
XX
AC AAH98714;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 571.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR P-PSDB; AAM24055.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 567-568; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 3467 BP; 796 A; 1012 C; 990 G; 669 T; 0 other;

Query Match 22.4%; Score 811.6; DB 22; Length 3467;
Best Local Similarity 64.1%; Pred. No. 1.2e-200;
Matches 1376; Conservative 0; Mismatches 714; Indels 56; Gaps 8;

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Qy     199 TGGGCACCACTAAGCTCCGGCTGGTGGGCCCAGAGAGCAAGC-CAGAGGAGGGCCGCCTG 257
Db     425 TGGCCAAGATTCAGCTGCGCCTGGCTGGGCAGAAGAGGAAGCACAGCGAGGGCCCGGGTG 484

Qy     258 GAGGTGCTGCACCAGGGCCAGTGGGGCACCGTGTGTGATGACAACTTTGCTATCCAGGAG 317
Db     485 GAGGTGTACTATGATGGCCAGTGGGGCACCGTGTGCGATGACGACTTCTCCATCCACGCT 544

Qy     318 GCCACAGTGGCTTGCCGCCAGCTGGGCTTCGAAGCTGCCTTGACCTGGCCCACAGTGCC 377
Db     545 GCCCACGTCGTCTGCCGGGAGCTGGGCTACGTGGAGGCCAAGTCCTGGACTGCCAGCTCC 604

Qy     378 AAGTACGGCCAAGGGGAGGGACCCATCTGGCTGGACAATGTGCGCTGTGTGGGCACAGAG 437
Db     605 TCCTACGGCAAGGGAGAAGGGCCCATCTGGTTAGACAATCTCCACTGTACTGGCAACGAG 664

Qy     438 AGCTCCTTGGACCAGTGCGGGTCTAATGGCTGGGGAGTCAGTGACTGCAGTCACTCAGAA 497
Db     665 GCGACCCTTGCAGCATGCACCTCCAATGGCTGGGGCGTCACTGACTGCAAGCACACGGAG 724

Qy     498 GACGTAGGGGTGATATGCCACCCCCGGCGCCATCGTGGCTACCTTTCTGAAACTGTCTCC 557
Db     725 GATGTCGGTGTGGTGTGCAGCGACAAAAGGATTCCTGGGTTCAAATTTGACAATTCGTTG 784

Qy     558 AATGCCC---TTGGGCCCCAGGGCCGGCGGCTGGAGGAGGTGCGGCTCAAGCCCATCCTT 614
Db     785 ATCAACCAGATAGAGAACCTGAATATCCAGGTGGAGGACATTCGGATTCGAGCCATCCTC 844

Qy     615 GCCAGTGCCAAGCAGCATAGCCCAGTGACCGAGGAGCCGTGGAGGTGAAGTATGAGGGC 674
Db     845 TCAACCTACCGCAAGCGCACCCCAGTGATGGAGGGCTACGTGGAGGTGAAGGAGGGCAAG 904

Qy     675 CACTGGCGGCAGGTGTGTGACCAGGGCTGGACCATGAACAACAGCAGGGTGGTGTGCGGG 734
Db     905 ACCTGGAAGCAGATCTGTGACAAGCACTGGACGGCCAAGAATTCCCGCGTGGTCTGCGGC 964

Qy     735 ATGCTGGGCTTCCCCAGCGAGGTGCCTGTCGACAGCCACTACTACAGGAAAGTCTGGGAT 794
Db     965 ATGTTTGGCTTCCCTGGGGAGAGGACATACAATACCAAAGTGTACAAAA----------- 1013

Qy     795 CTGAAGATGAGGGACCCTAAGTCTAGGCTGAAGAGCCTGACGAATAAGAACTCCTTCTGG 854
Db    1014 ---------------------------TGTTTGCCTCACGGAGGAAGCAGCGCTACTGG 1045

Qy     855 ATCCACCAGGTCACCTGCCTGGGGACAGAGCCCCACATGGCCAACTGCCAGGTGCAGGTG 914
Db    1046 CCATTCTCCATGGACTGCACCGGCACAGAGGCCCACATCTCCAGCTGCAAGCTGGGCCCC 1105

Qy     915 GCTCCAGCCCGGGGCAAGCTGCGGCCAG----CCTGCCCAGGTGGCATGCATGCTGTGGT 970
Db    1106 CAGGTGTCACTGGACCCCATGAAGAATGTTCACCTGCGAGAATGGGCTACCGGCCGTGGT 1165

Qy     971 CAGCTGTGTGGCAGGGCCTCACTTCCGCCCACCGAAGACAAAGCCACAACGCAAAGGGTC 1030
Db    1166 GAGTTGTGTGCCTGGGCAGGTCTTCAGCCCTGACGGACCCTCGAGATTCCGGAAAGCATA 1225

Qy    1031 CTGGGC--AGAGGAGCCGAGGGTGCGCCTGCGCTCCGGGGCCCAGGTGGGCGAGGGCCGG 1088
Db    1226 CAAAGCCAAGAGCAACCCCTGGTGCGACTGAGAGGCGGTGCCTACATCGGGGAGGGCCGC 1285

Qy    1089 GTGGAAGTGCTCATGAACCGCCAGTGGGGCACGGTCTGTGACCACAGGTGGAACCTCATC 1148
Db    1286 GTGGAGGTGCTCAAAAATGGAGAATGGGGGACCGTCTGCGACGACAAGTGGGACCTGGTG 1345

Qy    1149 TCTGCCAGTGTCGTGTGTCGTCAGCTGGGCTTTGGCTCTGCTCGGGAGGCCCTCTTTGGG 1208
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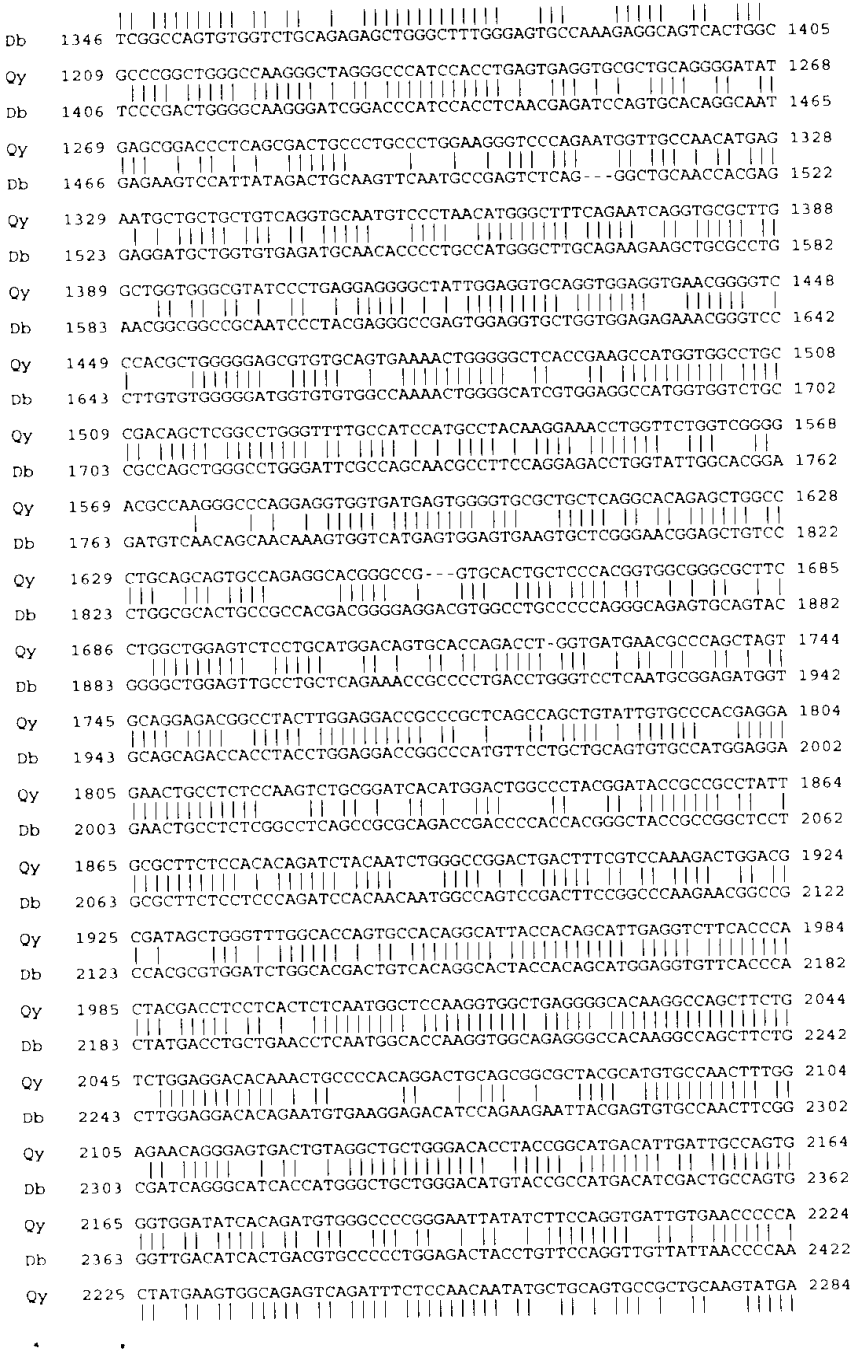
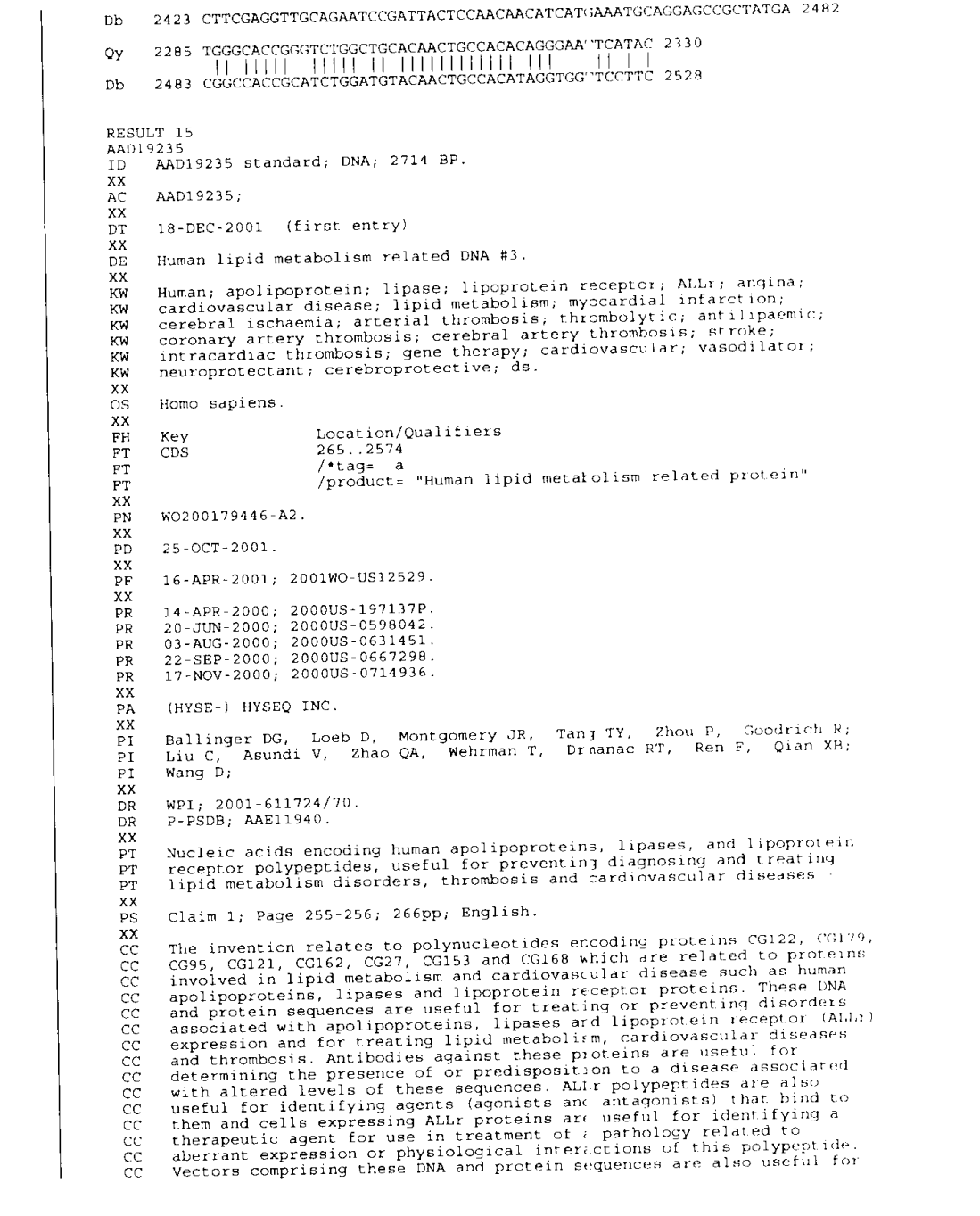
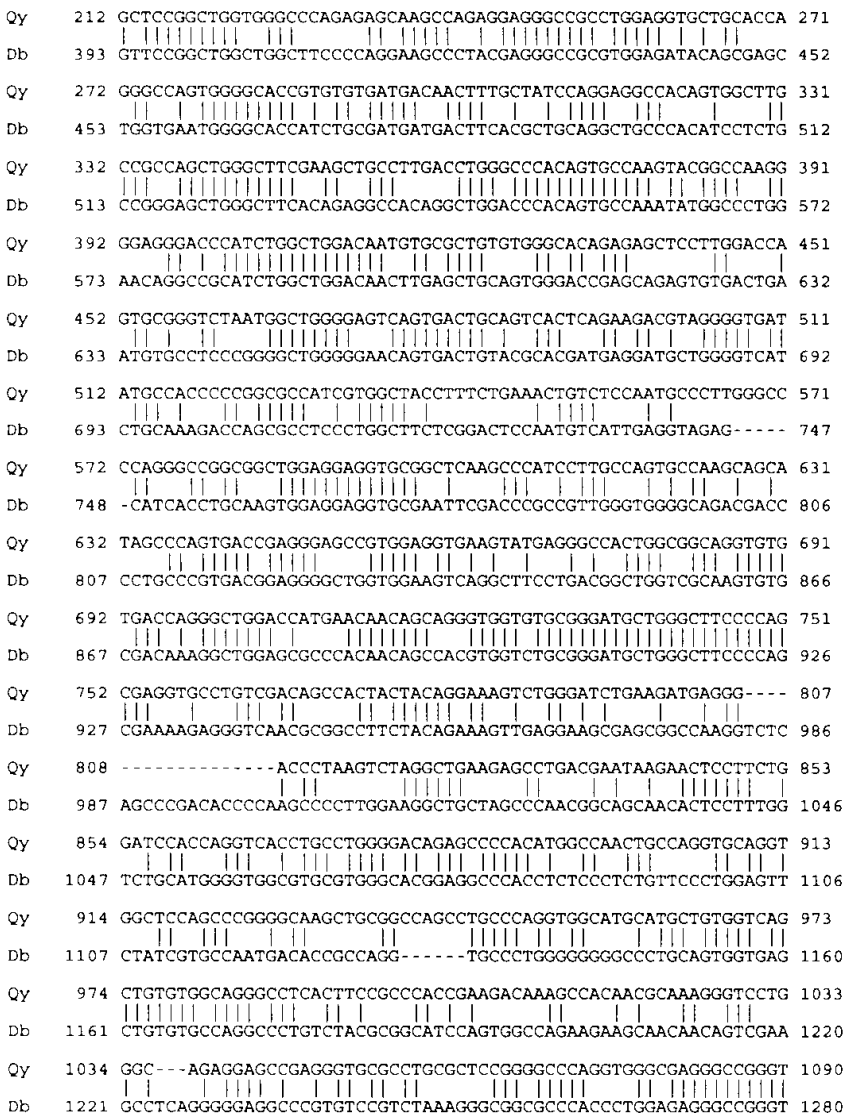


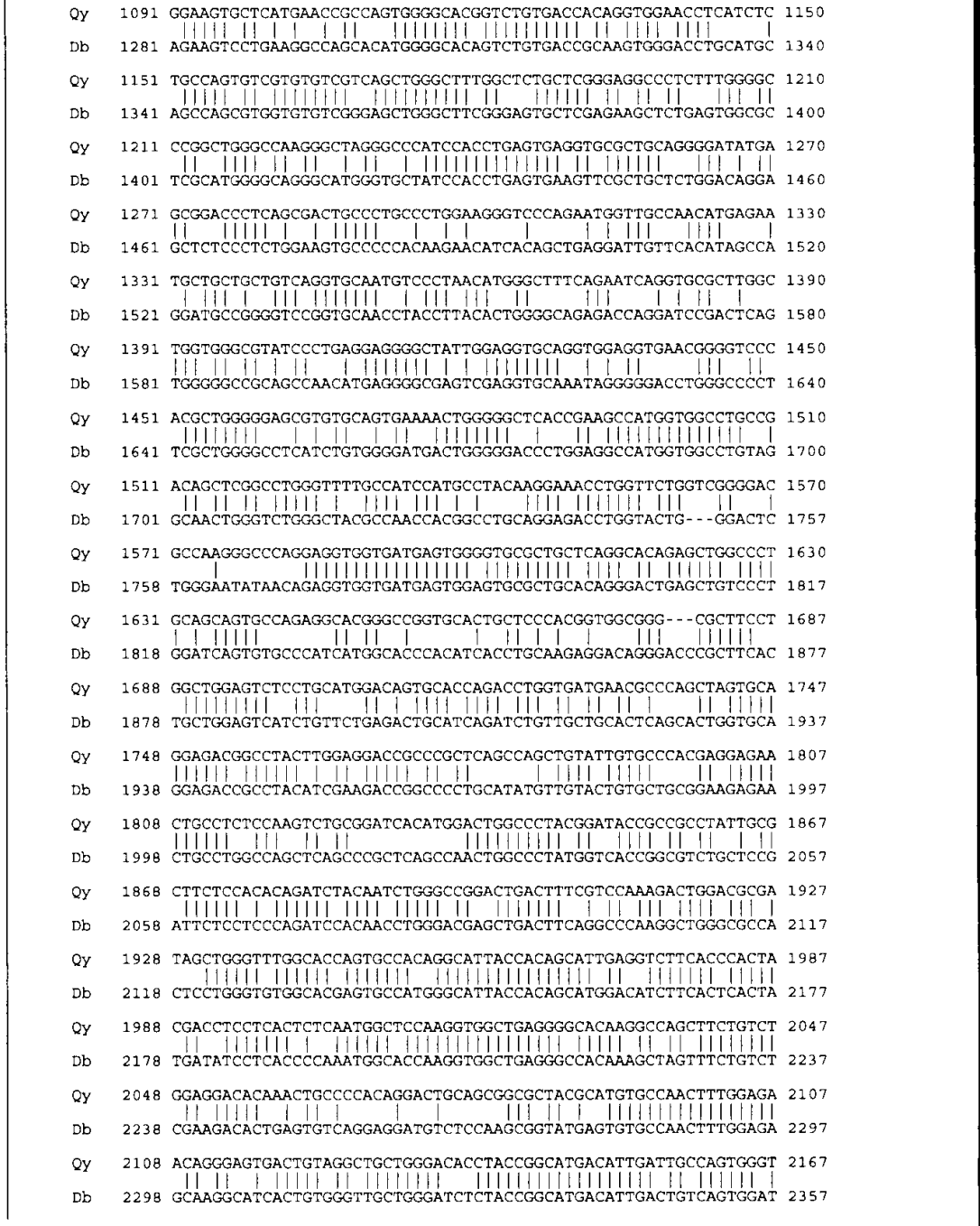


RESULT 15
AAD19235
ID AAD19235 standard; DNA; 2714 BP.
XX
AC AAD19235;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human lipid metabolism related DNA #3.
XX
KW Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina;
KW cardiovascular disease; lipid metabolism; myocardial infarction;
KW cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic;
KW coronary artery thrombosis; cerebral artery thrombosis; stroke;
KW intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
KW neuroprotectant; cerebroprotective; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 265..2574
FT /*tag= a
FT /product= "Human lipid metabolism related protein"
XX
PN WO200179446-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US12529.
XX
PR 14-APR-2000; 2000US-197137P.
PR 20-JUN-2000; 2000US-0598042.
PR 03-AUG-2000; 2000US-0631451.
PR 22-SEP-2000; 2000US-0667298.
PR 17-NOV-2000; 2000US-0714936.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;
PI Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;
PI Wang D;
XX
DR WPI; 2001-611724/70.
DR P-PSDB; AAE11940.
XX
PT Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
PT receptor polypeptides, useful for preventing diagnosing and treating
PT lipid metabolism disorders, thrombosis and cardiovascular diseases
XX
PS Claim 1; Page 255-256; 266pp; English.
XX
CC The invention relates to polynucleotides encoding proteins CG122, CG179,
CC CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins
CC involved in lipid metabolism and cardiovascular disease such as human
CC apolipoproteins, lipases and lipoprotein receptor proteins. These DNA
CC and protein sequences are useful for treating or preventing disorders
CC associated with apolipoproteins, lipases and lipoprotein receptor (ALLr)
CC expression and for treating lipid metabolism, cardiovascular diseases
CC and thrombosis. Antibodies against these proteins are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of these sequences. ALLr polypeptides are also
CC useful for identifying agents (agonists and antagonists) that bind to
CC them and cells expressing ALLr proteins are useful for identifying a
CC therapeutic agent for use in treatment of a pathology related to
CC aberrant expression or physiological interactions of this polypeptide.
CC Vectors comprising these DNA and protein sequences are also useful for

CC producing ALLr proteins. The nucleic acids and polypeptides of the
CC invention are also useful for the treatment of occlusive cardiovascular
CC diseases, myocardial infarction, cerebral ischaemia, angina, arterial
CC thrombosis, coronary artery thrombosis and cerebral artery thrombosis
CC or intracardiac thrombosis and stroke. The nucleotides of the invention
CC are used in gene therapy. The present sequence is human DNA encoding a
CC protein related to proteins involved in lipid metabolism.
XX
SQ Sequence 2714 BP; 560 A; 761 C; 877 G; 516 T; 0 other;

Query Match 21.8%; Score 787.4; DB 22; Length 2714;
Best Local Similarity 62.7%; Pred. No. 2.1e-194;
Matches 1343; Conservative 0; Mismatches 761; Indels 39; Gaps 6;





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Qy    2168 GGATATCACAGATGTGGGCCCCGGGAATTATATCTTCCAGGTGATTGTGAACCCCCACTA 2227
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Db    2358 TGACATCACGGATGTGAAGCCAGGAAACTACATTCTCCAGGTTGTCATCAACCCAAACTT 2417

Qy    2228 TGAAGTGGCAGAGTCAGATTTCTCCAACAATATGCTGCAGTGCCGCTGCAAGTATGATGG 2287
           |||||| |||||||    || ||  ||||||||     || | ||    |||||| |||||||| 
Db    2418 TGAAGTAGCAGAGAGTGACTTTACCAACAATGCAATGAAATGTAACTGCAAATATGATGG 2477

Qy    2288 GCACCGGGTCTGGCTGCACAACTGCCACACAGGGAATTCATAC 2330
           ||  |  ||||| ||||||||||||||||  ||  || | | |
Db    2478 ACATAGAATCTGGGTGCACAACTGCCACATTGGTGATGCCTTC 2520
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